

Table 70: Comparative Sequences relating to SAG 1280

ATACCTTTATTGAGTTTGAAAACCTTGGAAATTGATTTCTTTTTTGTGGATGAGGCTCATC
 ACTTCAAGAATATCCGTCCTAATCACTGGACTTGGGAATGTAGCTGGAATCACCACACAA
 CTTCTAAAAAGAACCGTGGATATGGAGATGAAGGTGAGACAAAGTACAGGCAGAGCATGGAG
 ATAGAAATGTCGTTTTTGGCAGCAGGAACACCAAGTTCTAACTCTATTAGTGAACCTTTCA
 CCATGATGGATTACATTCACCTGATGTCTTGGAACGATACCTGGTATCAAATTTTGACT
 CCTGGGTTGGGGCTTTTGGGAATATCGAAAACCTCCATGGAAGTACCCCGACAGGAGATA
 AGTACCAACCCAAAGAACCGTTCAAGAAATTTGTCAACCTTCCTGAACTCATGCGAATCT
 ACAAGGAACTGCCGATATTAGACCTCAGACATGCTTGATTTACCAGTACCAGGAAAGCTA
 AGATTATTGCGGTGGAAAGCGAGTTAACGCAAGCTCAGAAATCTATTGGAAAGAGCTGG
 TAAAGCGTTGAGACGCTATCAAGTCAAGTGTGTTGATCCAAGTAGAGATAACATGCTTA
 AAATCACAGGAGAAGCCAGAAAACCTAGCTATTGATATGCGGTTGATTGACCCCTACTTACT
 CCTTATCGGATATAGCAGAAATCCTTCAAGTAGTCCGATAATGTCGAGCGGATTTACCGTG
 ATGGAGCTGGAGACAAGCCACTCAGATGATTTTCTCAGATATTGGAACCCCTAAAAGTA
 AGGAAGAAGGGTTTGTATGTCTACAATGAACCTTAAGGACTTGTTTGTGCGATCGAGGGATC
 CAAAAGAGAAATTTGCTTGTCCATGATGCCAATCTGATGAGAAGAAAACTCTCTGT
 CAGCAAGGTCAATAGTGGAGAACTAGCTTATGATATGCGGTTGATTGACCCCTACTTACT
 CAGGATTAACCTGCAATCTCGCATGAAAGCTGTCCACTATTAGACGTTCCCTGGAGGC
 CCTCAGACATTTGTCAGCGAAATGGACGACTAATTGACAAAGAAACATGCACCAGGAGG
 TAGATATTTATCACTATATTACTAAAGGGAGCTTTGACAATTACCTCTGCGCAGACGCGAG
 AGAATAAGCTAAAGTATATCACCCAGATAATGACCTCAAAGATCCTGTGAGATCAGCTG
 AAGACATTGATGAACAACCATGACCCGCTCAGACTTTAAGGCATTGGCAACTGGGAACC
 CTTATCTCAAACCTCAAATGGAGTTGGAAAATGAACCTGACAGTTTATAGAGAAATCAAAC
 GAGCCTTTAATCGCTCAAAGACGAGTATCGCCATACCATTTCCTATAGCGAGAAGCACCC
 TCCTTATATGGAAAACCGTTGAGTCAATATGATAAAGATATTGCCCAATCTTTGGCAA
 CCAAGTCGCAAGATTTTGTGATGCGATTGACAATCAAGCAATGGATAATCGTGCTGAAG
 CTGGGACTATCTGCGAAAACCTTACCTATAAAGCGCTCAGAGACCAAGGAAGTCAAGTA
 CACTTGGCAGCTTTAGAGGATTTGATTTAAAATGACTACAGGCTGCTAGTGAAGCCCT
 TACCAGAAACCTTTCTTTAATGATTTGATGGTATACCAAGTACTGTCGCCCTTGATT
 TGAATCAGACCTGGGAACCATTCACCGGATTAGTAATGCACTGACCATATTATAGATG
 ACCAAGAAAAGACGCAAGAGCTGTTAAAGGATTTAAAAGATAAGCTACAGGATAGCCAAAG
 TAGAAGTTGATAAAGTCTTTCCAAAGGAAGAGGACTATCAGCTTGTAAAGGCTAAGTATG
 ATGTTTTAGCTCCCTTGGTTGAAAAGAAAGCAGAGATTGAAGAGATAGATGCAGCTTTGG
 CCAAGTTTAGTGAAGATACAACCCCAAAGGAAGCAACAATAGCACTCGAGATA

SEQ ID. NO. 7002

STRAIN H36B

GGAGGGAAAAATGAATCAAGAAGTCTTACTACAATGAT
 GAGAGCCACTATTCCTCGTGTAGAGCCCTTGCTTGAGGCATTTTATATTT
 ACCAAGCAGAGCATTTTGTATGAGGAGTGGGACTAGTCTTATTATCAGTTT
 ATGACCAATAGGCAAGAAAATAAATAAGTCTGTTCAAGTACTTCACTTTGA
 GACAGATGTTTCAAGCTTTTGTCCAGGCTAGTCTTATGATGACTGCTCATG
 ATCTATTGACCTATAACAAGTTTTCGGCCAAAGTGGTCTTCAAAAACCTA
 GATAAATCTATCGCCGCTGAAAAAACTTTGGTGTAGAAAGTGGCCTTGT
 CAATCTGGCCACTCGTTTTCAATTTTGGATTCCAATGGACACTACCAA
 CCATATCGCCCGATTCACTCTTACAAAAGAGTAGGGGAGCTAAATTTGGTC
 AATGTGTATCGTGTGGCTAATAATTTAGCGGATCGTATTAGTCCGAGATAT
 TGAACAGTTTCTCTAACTTACGAGCCTGAGCTTGAACCTAGAGCTGATG
 AAAGTGTCTAGAAAATGAAGAACTGTTGATGAGCAGCAAAAAGAGTGT
 CATCAAGCAATATCTTTGAGAGAGAGGGCTCTCTGTTTATTGCTAGTTT
 GGATGTAGATTTGTCTCAACTAGATGTTCAAATAGGAAAACCAAGTCACT
 TGCCAGCTTATGAAGAGTTATCCTTACGACGTAATTTGAGATTCTAACA
 TATTTTGACCAAAATCGAAATGAACGTTCCAAAGTCCCAAGTTTGTAGACG
 AGGTGATTTTGACACAGAGATGGAAATGACACCAAGTCTTTGATGGCGAGG
 AATTAATCTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAAACGA
 ACGCTGACTACAGTCAAGAAAAGGAATTAGAAAATAATGGACAAGCCAT
 TAGGATAGAAAATCAAGAAAATTTGACTCAGCTAsGkATTGrTTTATCTC
 AGTTTGACCCAGACCGAGTCCGATTTTATTGKATGAGCAGGTCGTYyT
 CGTTTAWAWAATGACAGACTTGTCTCACTAGGTGGTTATCCAAAAGCCCT
 GGTAACTCAACTAGCCCTTGGCAGAGAACTACTCCAAATGGGACTAAGTCT
 ATGAAAAGGTTGAATTTTCTTTGGTAGCCAGCTTCCATTGAAGAGCTG
 CGACAAGTTGCCCTACGCCCTTTTACACCAAGAAGTCCAGCAGAGAAGATC
 GGAGCAATTTGAAAAAGATAAAGGTAATCAGCCAGATTTAATCTCAGAG
 ATTGAAAAAGCAAGCTAGAGAAAAGCTGAGGGAAAAGAAAGTAGTTGATGAA
 GAATTCGCGGAAAATCCACTGGTTAGAGAGTATTGGACACTTATCCTCT
 GGGGTCAITGGTTTCTATAAGGGACAGGACTTTGAGTCAATGTCGCTCA
 GCGATGCTCGATGAAACGGTTTGAATTCGGATTGAGTGTAGTCAATGACTTT
 TCGGATATCATTGAAACAAAATCCAGTTCTTTATGTGAGGACCTGGGAAGA
 AGTCAGTCAGGCACTTCACTCAGCCAAAGGCAGAACCAACACAGAGTTAG
 AAGAAGCGGACCAAGAATTAACCTATTCTCAATTTCTGGAAGAGGAGCTA
 GTTCAGAGTATTGGACTATTGGAAACAGATGATTGAGAAAATGGTCATAA
 CGATACTGATCTTGAAGAAAAGATAAATCAAATTCCTGAAGAGGAAGTGC
 TCGAAACAATTCAGAGATTCCAGTAAACGGACTTTTATTTTCCAGAAGAT
 TTGACGGACTTTTATCCTTAAGACTGCTAGAGATAAGGTTGAGACAAAACAT
 TGTGGCCATTCTTTGGTAAAAAATCTAGAAGTAGAGCACCGCAATGCTT
 CACCAGTGAACAAGAAGCTCTTGGCAAGTATGTAGGCTGGGGTGGACTA
 GCCAATGAATTTTGTGATGACTATAATCCAAAATTTTCAAGGAACGAGA
 AGAAGTGAAGAGCTAGTCAAGATAAAGAGTATTCCGATATGAAACAGT
 CCTCCCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGATGATGTTGG
 GATAAGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCTTAGATCCTTC
 CATGGGAACAGGAAATTTCTTTGCGGCTATGCCAAAACACTTAAGAGAAA
 AGAGTGAAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCC
 AAACACCTTCATCCAAATAGTCAATTTGAATTAAGGATTTGAGACGGT
 GGCTTTAACGCAATAGTTTGTATTGGTGAATTTCAAATGTGCCCTTTG

Table 70: Comparative Sequences relating to SAG 1280

CCAATATACGAAATGCGGATAATAGGTACGATAGGCCCTTACATGATTCA
GACTACTTTGTCAAAAAGTCACTTGTATTTGCTTCATGATGGTGGACAAGT
AGCGATTATCTCTTCCACAGGAACCTATGGATAAGCGAACAGAAAAATCATCT
TACAAGATATTCGTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCT
GACTCTGCCCTTAAAGGCCATTGCAGGAACGAGTGTCAACAACGGATATGTT
ATTCTTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCCT
TTTCAGGTTCCATTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCCT
TATTTTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTCAG
GAATTTTAAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGA
TTGCAAGTGTGAAACAGCTCTAAATCACGTTAAGGCCCCAGAGAGATT
GATAGAAATGAGGTCATCATTAACCCAGATGTGTTGACCAACAAGTCAA
TGATACCTCCATTCAGCTGAAATGAGGGAAAAATCTAGGTCACTACAGTT
TTGGTTATCAGGGGCTACAGTTTACTATCGAGATAACAAAGGCATTCGA
GTCGGAACCAAGACGGAAGAAATCAGTTACTATGTCCGATGAAGAG

SEQ ID. NO. 7003
STRAIN 18RS21

GnAGGGAAAATGAATCAAGAAGTCTTACTACAAATGATGAGA
GCCACTATTCCCTCGTGATAGAGCCTTGCTTGAGGCATTTTATATTACCA
AGCAGAGCATTGATGAGGAGTGGGATAGTCTTATTTCATCAGTTTATGA
CCAATAGGCAAGAAAATAAATAAGTCTGTTCAAGTACTTCACTTTGAGACA
GATGTTTCCAGCTTTTGTCCAGGCTAGTCTTATGATACTGCTCATGATCT
ATTGACCTATACACAAGTTTTCGGCCAAAGTGGTCTTCAAAAAGTATGATA
AATATACGCCCTCTGAAAAAACTTGGTGATAGAAGTGGCCTTGTTCAT
CTGGCCACTCGTPTTCAATTTATGGATTCCAAATGGACACTACCAACCAT
ATCGCCGATTCACCTTACAAAAGAGTAGGGGAGCTAAATTTGGTCAATG
TGTATCGTGTGGCTAATAAATTTAGCGGATCGTATTAGTCGAGATAITGAA
CAGTTTCTTAACTTACGAGCCTGAGCTTGAACACTAGAGCTGATGAAAC
TGTTCTAGAAAAATGAAGAAACTGTTGATGAGCACAACAAAGTGTTCATC
AAGCAATATCTTTTTCGAGAAGAGGGCTCTCTGGTTATTGCTAGTTTGGAT
GTAGATTTGTTCTCAACTAGATGTTCAAATAGGAAAAACAGTTCATCTGCC
AGCTTATGAAGAGTTTCTTACGAGCTAAATTTGAGATTCTAACATATT
TTGACCAAATTCGAAATGAACGTTCCAAAGTCCCAAGTTTGTAGCAGGTT
GATTTTGACACAGAGATGGAATGACACCAGTCTTTGATGGCGAGGAATT
ACTTACTTATCTCGAAGCTGATGGCAGTCCCTATGAGCTGAAACGAAACGC
TGACTACAGTcGAAGAAAAGGAAATAGAAAAAATTTGGACAAGCCATTAGG
ATAGAAAAATCAAGAAAAATGACTCAGCTAGGATTTGATTTATCTCAGTT
TGACCCAGACCGAGTCCGGTATTTTATTTGATGACAGCAGGTCGTTTTCGTT
TAAAAAATGACAGCCTTGCTTTACTAGGTTGGTTATCCCAAAGCCTCGGTA
ACTCAACTAGCCCTTGGCAGACAGAACTACTCCAAATGGGACTAAGTCATGA
AAAGTTGAATTTTCTTTGGTAGCCAGCTTTCATTGGAAGAGCTGCGAC
AAGTTGCCTACGCCCTTTTACACCAAGAACTCAGCAGAGAAGATGCGGAG
CAATTTGAAAAAAGATAAAGGTAATCAGCCAGATTTAACTCTCAGAGATTG
GAAAGCAAGCTAGAGAAAGCTGAGGGAAAAGAGTAGTTGATGAAGAAT
TCGCGGAAAATCCACTGGTTCAGAGAGTATTGGACACTTATCCTCTGGGG
TCATTGGTTTCTATAAGGGACAGGACTTTGAGGTCATGTCGGTCAGCGA
TGCTCGATTGAAACGGTTTGAATTCGGATTGAGTTAGTCAATGACTTTTCG
ATATCATTGAACAACAAATCCAGTTCTTALGTGAGGACCTGGGAAGAAATC
AGTCAGGCACTTATCAGCCAAAGGCAGAACCAACAAACAGAGTTAGAAGA
AGCGGACCAAGAATTAACCTATTCTCATTCTGGAAGAGGAGCCAGTTC
AGAGTATTGGACTATTGGAAACAGATGATTGAGAAAAATGGTCAATACGAT
ACTGATCTTGAAGAAACAGATAAATCAAATTCCTGAAAGAGGAGTCTGCGA
AACTAATCCAGAGATTCCAGTAACGGACTTTTATTTTCCAGAAGATTGGA
CGGACTTTTATCTTAAGACTGCTAGAGATAAGGTTGAGACAAACATTTGTG
GCCATTCGTTTGGTAAAAAATCTAGAAGTAGAGCACCAGCAATGCTTCACC
AAGTGAAACAGAACTCCTTGCCAAAGTATGTTAGGCTGGGGTGGACTAGCCA
ATGAATTTTGTGATGACTATAATCCAAAATTTTCTAAGGaaACGAGAAGAA
CTGAAGAGCCTAGTCAAGATAAAGAGTATTCCGATATGAAACAGTCCCTC
CCTGACAGCCTATTACACAGACCCATCCCTGATCCGTGATGTTGGGATA
AGTTGGAAGAGATGGCTTTACAGGTGGCAAAATCTTAGATCCTTCCATG
GAAACAGGGAATTTCTTGGGCTATGCAAAAACACTTAAGAGAAAAGAG
TGAGTTGATGGCGTAGAGTTAGATACTATTACAGGAGCTATTGCCAAAC
ACCTTCATCCCAATAGTCATATTGAAATTAAGGGATTTGAGACGGTGGCT
TTTTAACGACAATAGTTTGAATTTGGTGAATTCAAATGTGCCCTTTGCCAA
TATAAGAAATGCGGATAATAGGATACGATAGGCCCTTACATGATTTATGACT
ACTTTGTCAAAAAGTCACTTGAATTTGCTTCATGATGGTGGCAAGTAGCG
ATTATCTCTTCCACAGGAACCTATGGATAAGCGAACAGAAAAATCTTACA
AGATATTGTTGAGACAACCTGAATTTCTTGGTGGGGTTCGACTGCCTGACT
CTGCCCTTAAAGGCCATTGCAGGAACGAGTGTCAACAACGGATATGTTATTCT
TTCCAGAAACACTTAGACAAGGGATATGTGGCAGACGATTTAGCCCTTTTC
AGGTTCCATTCGCTATGACAAGGATAGTCGCATTTGGCTCAATCTTATT
TTGATGGAGAATACAATAGCCAGGTGCTAGGAACCTACGAGGTCAGGAAT
TTTTAACGGAGGAACACTTTCTGTTAAGGGGACTAGTGATGACTTGTATGTC
AAGTGTGTAACACAGCTCTAAATCACGTTAAGGCCCCAGAGAGAGATTGATA
GAAATGAGGTCATCATTAACCCAGATGTGTTGACCAACAAGTCAATGAT
ACCTCCATTCAGCTGAAATGAGGGAAAAATCTAGGTCACTACAGTTTGG
TTATCAGGGGCTACAGTTTACTATCGAGATAACAAAGGCATTCGAGTGC
GAACCAAGACGGAAGAAATCAGTTACTATGTCCGATGAAGAG

MSA Alignment Results: Pretty output
PRETTY of: /biotmp/msa31161.2{*} June 20, 2002 10:41 ..

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dNt_2603}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327d_18RS21}	GnAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
msa31161.2{327dNT_H36B}	GgAGGGAAAA	TGAATCAAGA	AGTCTTACTA	CAAATGATGA	GAGCCACTAT
Consensus	*-*****	*****	*****	*****	*****
	51				100
msa31161.2{327dNt_2603}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327d_18RS21}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
msa31161.2{327dNT_H36B}	TCCTCGTGAT	AGAGCCTTGC	TTGAGGCATT	TTTATATTAC	CAAGCAGAGC
Consensus	*****	*****	*****	*****	*****
	101				150
msa31161.2{327dNt_2603}	ATTTTGTATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327d_18RS21}	ATTTTGTATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
msa31161.2{327dNT_H36B}	ATTTTGTATGA	GGAGTGGGAT	AGTCTTATTC	ATCAGTTTAT	GACCAATAGG
Consensus	*****	*****	*****	*****	*****
	151				200
msa31161.2{327dNt_2603}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
msa31161.2{327d_18RS21}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
msa31161.2{327dNT_H36B}	CAAGAAATAA	ATAAGTCTGT	TCAAGTACTT	CACTTTGAGA	CAGATGTTTC
Consensus	*****	*****	*****	*****	*****
	201				250
msa31161.2{327dNt_2603}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327d_18RS21}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
msa31161.2{327dNT_H36B}	AGCTTTTGTC	CAGGCTAGTC	CTTATGATAC	TGCTCATGAT	CTATTGACCT
Consensus	*****	*****	*****	*****	*****
	251				300
msa31161.2{327dNt_2603}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAAACTAGA	TAAACTATCG
msa31161.2{327d_18RS21}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAAACTAGA	TAAACTATCG
msa31161.2{327dNT_H36B}	ATACACAAGT	TTTCGGCCAA	AGTGGTCTTC	AAAAACTAGA	TAAACTATCG
Consensus	*****	*****	*****	*****	*****
	301				350
msa31161.2{327dNt_2603}	CCGTCFGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327d_18RS21}	CCGTCFGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
msa31161.2{327dNT_H36B}	CCGTCFGAAA	AAAACCTGGT	GATAGAAGTG	GCCTTGTTCA	ATCTGGCCAC
Consensus	*****	*****	*****	*****	*****
	351				400
msa31161.2{327dNt_2603}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327d_18RS21}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
msa31161.2{327dNT_H36B}	TCGTTTTCAA	TTATTGGATT	CCAATGGACA	CTACCAAACC	ATATCGCCGG
Consensus	*****	*****	*****	*****	*****
	401				450
msa31161.2{327dNt_2603}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTTGGTCAA	TGTGTATCGT
msa31161.2{327d_18RS21}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTTGGTCAA	TGTGTATCGT
msa31161.2{327dNT_H36B}	ATTCACCTCT	ACAAAAGAGT	AGGGGAGCTA	ATTTGGTCAA	TGTGTATCGT
Consensus	*****	*****	*****	*****	*****
	451				500
msa31161.2{327dNt_2603}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327d_18RS21}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
msa31161.2{327dNT_H36B}	GTGGCTAATA	ATTTAGCGGA	TCGTATTAGT	CGAGATATTG	AACAGTTTCT
Consensus	*****	*****	*****	*****	*****
	501				550
msa31161.2{327dNt_2603}	CTTAACTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327d_18RS21}	CTTAACTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
msa31161.2{327dNT_H36B}	CTTAACTTAC	GAGCCTGAGC	TTGAAACTAG	AGCTGATGAA	ACTGTTCTAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa31161.2{327dNt_2603}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327d_18RS21}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
msa31161.2{327dNT_H36B}	AAAATGAAGA	AACTGTTGAT	GAGCACAAAA	CAAGTGTTC	TCAAGCAATA
Consensus	*****	*****	*****	*****	*****
	601				650
msa31161.2{327dNt_2603}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATTT
msa31161.2{327d_18RS21}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATTT
msa31161.2{327dNT_H36B}	TCITTTTCGAG	AAGAGGGCTC	TCITGGTTATT	GCTAGTTTGG	ATGTAGATTT
Consensus	*****	*****	*****	*****	*****
	651				700
msa31161.2{327dNt_2603}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327d_18RS21}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
msa31161.2{327dNT_H36B}	GTCTCAACTA	GATGTTCAAA	TAGGAAAAAC	CAGTCATCTG	CCAGCTTATG
Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

	701				750
msa31161.2{327dNt_2603}	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
msa31161.2{327d_18RS21}	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
msa31161.2{327dNT_H36B}	AAGAGTTATC	CTTACGACGT	AAATTTGAGA	TTCTAACATA	TTTTGACCAA
Consensus	*****	*****	*****	*****	*****
	751				800
msa31161.2{327dNt_2603}	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
msa31161.2{327d_18RS21}	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
msa31161.2{327dNT_H36B}	ATTTCGAAATG	AACGTTCCAA	AGTCCCAAGT	TTTAGACGAG	GTGATTTTGA
Consensus	*****	*****	*****	*****	*****
	801				850
msa31161.2{327dNt_2603}	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
msa31161.2{327d_18RS21}	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
msa31161.2{327dNT_H36B}	CACAGAGATG	GAAATGACAC	CAGTCTTTGA	TGGCGAGGAA	TTACTTACTT
Consensus	*****	*****	*****	*****	*****
	851				900
msa31161.2{327dNt_2603}	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
msa31161.2{327d_18RS21}	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
msa31161.2{327dNT_H36B}	ATCTCGAAGC	TGATGGCAGT	CCCTATGAGC	TGAAACGAAC	GCTGACTACA
Consensus	*****	*****	*****	*****	*****
	901				950
msa31161.2{327dNt_2603}	GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
msa31161.2{327d_18RS21}	GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
msa31161.2{327dNT_H36B}	GTCGAAGAAA	AGGAATTAGA	AAAAATTGGA	CAAGCCATTA	GGATAGAAAA
Consensus	*****	*****	*****	*****	*****
	951				1000
msa31161.2{327dNt_2603}	TCAAGAAAAA	TTGACTCAGC	TAgGgATTGa	TTTATCTCAG	TTTGACCCAG
msa31161.2{327d_18RS21}	TCAAGAAAAA	TTGACTCAGC	TAgGgATTGa	TTTATCTCAG	TTTGACCCAG
msa31161.2{327dNT_H36B}	TCAAGAAAAA	TTGACTCAGC	TAsGkATTGr	TTTATCTCAG	TTTGACCCAG
Consensus	*****	*****	*_*_*_*_*_*_*_*	*****	*****
	1001				1050
msa31161.2{327dNt_2603}	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTCGTtTTCG	TTTAAaAAAT
msa31161.2{327d_18RS21}	ACCGAGTCGG	TATTTTATTG	gATGCAGCAG	GTCGTtTTCG	TTTAAaAAAT
msa31161.2{327dNT_H36B}	ACCGAGTCGG	TATTTTATTG	kATGCAGCAG	GTCGTyyTTCG	TTTAAwAAAT
Consensus	*****	*****	*_*_*_*_*_*_*_*	*****	*****
	1051				1100
msa31161.2{327dNt_2603}	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
msa31161.2{327d_18RS21}	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
msa31161.2{327dNT_H36B}	GCAGACCTTG	CTTtACTAGG	TGGTTATCCC	AAAGCCTCGG	TAACCTCACT
Consensus	*****	*_*_*_*_*_*_*_*	*****	*****	*****
	1101				1150
msa31161.2{327dNt_2603}	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
msa31161.2{327d_18RS21}	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
msa31161.2{327dNT_H36B}	AGCCCTTGCG	ACAGAACTAC	TCCAAATGGG	ACTAAGTCAT	GAAAAGGTTG
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa31161.2{327dNt_2603}	AAITTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
msa31161.2{327d_18RS21}	AAITTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
msa31161.2{327dNT_H36B}	AAITTTTCTT	TGGTAGCCAG	CTTCCATTG	AAGAGCTGCG	ACAAGTTGCC
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa31161.2{327dNt_2603}	TACGCCTTTT	TatACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
msa31161.2{327d_18RS21}	TACGCCTTTT	TacACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
msa31161.2{327dNT_H36B}	TACGCCTTTT	TAcACCAAGA	ACTCAGCAGA	GAAGATGCGG	AGCAATTTGA
Consensus	*****	*_*_*_*_*_*_*_*	*****	*****	*****
	1251				1300
msa31161.2{327dNt_2603}	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
msa31161.2{327d_18RS21}	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
msa31161.2{327dNT_H36B}	AAAAGATAAA	GGTAATCAGC	CAGATTTAAC	TCTCAGAGAT	TGGAAAAGCA
Consensus	*****	*****	*****	*****	*****
	1301				1350
msa31161.2{327dNt_2603}	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGGAA
msa31161.2{327d_18RS21}	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGGAA
msa31161.2{327dNT_H36B}	AGCTAGAGAA	AGCTGAGGGA	AAAGAAGTAG	TTGATGAAGA	ATTTCGCGGAA
Consensus	*****	*****	*****	*****	*****
	1351				1400
msa31161.2{327dNt_2603}	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
msa31161.2{327d_18RS21}	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
msa31161.2{327dNT_H36B}	AATCCACTGG	TTCAGAGAGT	ATTGGACACT	TATCCTCTGG	GGTCATTGGT
Consensus	*****	*****	*****	*****	*****

Table 70: Comparative Sequences relating to SAG 1280

		1401			1450
msa31161.2	{327dNt_2603}	TTCTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC
msa31161.2	{327d_18RS21}	TTCTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC
msa31161.2	{327dNT_H36B}	TTCTATAAG	GGACAGGACT	TTGAGGTCAT	GTCGGTCAGC
	Consensus	*****	*****	*****	*****
		1451			1500
msa31161.2	{327dNt_2603}	TGAACGGTTT	GATTCGGATT	GAGTTAGTCA	ATGACTTTTC
msa31161.2	{327d_18RS21}	TGAACGGTTT	GATTCGGATT	GAGTTAGTCA	ATGACTTTTC
msa31161.2	{327dNT_H36B}	TGAACGGTTT	GATTCGGATT	GAGTTAGTCA	ATGACTTTTC
	Consensus	*****	*****	*****	*****
		1501			1550
msa31161.2	{327dNt_2603}	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG
msa31161.2	{327d_18RS21}	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG
msa31161.2	{327dNT_H36B}	GAACAAAATC	CAGTTCCTTA	TGTGAGGACC	TGGGAAGAAG
	Consensus	*****	*****	*****	*****
		1551			1600
msa31161.2	{327dNt_2603}	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA
msa31161.2	{327d_18RS21}	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA
msa31161.2	{327dNT_H36B}	ACTTCATCAG	CCAAAGGCAG	AACCACAAAC	AGAGTTAGAA
	Consensus	*****	*****	*****	*****
		1601			1650
msa31161.2	{327dNt_2603}	AAGAATTAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT
msa31161.2	{327d_18RS21}	AAGAATTAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT
msa31161.2	{327dNT_H36B}	AAGAATTAAA	CCTATTCTCA	TTTCTGGAAG	AGGAGCAGT
	Consensus	*****	*****	*****	*****
		1651			1700
msa31161.2	{327dNt_2603}	GGACTATTGG	AACCAGATGA	TTTCAGAAAAT	GGTCATAACG
msa31161.2	{327d_18RS21}	GGACTATTGG	AACCAGATGA	TTTCAGAAAAT	GGTCATAACG
msa31161.2	{327dNT_H36B}	GGACTATTGG	AACCAGATGA	TTTCAGAAAAT	GGTCATAACG
	Consensus	*****	*****	*****	*****
		1701			1750
msa31161.2	{327dNt_2603}	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC
msa31161.2	{327d_18RS21}	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC
msa31161.2	{327dNT_H36B}	TGAAGAAACA	GATAATCAAA	TTCTGAAGA	GGAAGTCGTC
	Consensus	*****	*****	*****	*****
		1751			1800
msa31161.2	{327dNt_2603}	CAGAGATTC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT
msa31161.2	{327d_18RS21}	CAGAGATTC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT
msa31161.2	{327dNT_H36B}	CAGAGATTC	AGTAACGGAC	TTTTATTTTC	CAGAAGATTT
	Consensus	*****	*****	*****	*****
		1801			1850
msa31161.2	{327dNt_2603}	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG
msa31161.2	{327d_18RS21}	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG
msa31161.2	{327dNT_H36B}	TATCCTAAGA	CTGCTAGAGA	TAAGGTTGAG	ACAAACATTG
	Consensus	*****	*****	*****	*****
		1851			1900
msa31161.2	{327dNt_2603}	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA
msa31161.2	{327d_18RS21}	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA
msa31161.2	{327dNT_H36B}	TTTGGTAAAA	AATCTAGAAG	TAGAGCACCG	CAATGCTTCA
	Consensus	*****	*****	*****	*****
		1901			1950
msa31161.2	{327dNt_2603}	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC
msa31161.2	{327d_18RS21}	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC
msa31161.2	{327dNT_H36B}	AAGAACTCCT	TGCCAAGTAT	GTAGGCTGGG	GTGGACTAGC
	Consensus	*****	*****	*****	*****
		1951			2000
msa31161.2	{327dNt_2603}	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG
msa31161.2	{327d_18RS21}	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG
msa31161.2	{327dNT_H36B}	TTTGATGACT	ATAATCCAAA	ATTTTCTAAG	GAACGAGAAG
	Consensus	*****	*****	*****	*****
		2001			2050
msa31161.2	{327dNt_2603}	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC
msa31161.2	{327d_18RS21}	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC
msa31161.2	{327dNT_H36B}	CCTAGTCACA	GATAAAGAGT	ATTCGGATAT	GAAACAGTCC
	Consensus	*****	*****	*****	*****
		2051			2100
msa31161.2	{327dNt_2603}	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA
msa31161.2	{327d_18RS21}	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA
msa31161.2	{327dNT_H36B}	CCTATTACAC	AGACCCATCC	CTGATCCGTC	AGATGTGGGA

Table 70: Comparative Sequences relating to SAG 1280

Consensus	*****	*****	*****	*****	*****
	2101				2150
msa31161.2{327dNt_2603}	AGAGATGGCT	TTACAGGTGG	CAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327d_18RS21}	AGAGATGGCT	TTACAGGTGG	CAAATCCTA	GATCCTTCCA	TGGGAACAGG
msa31161.2{327dNT_H36B}	AGAGATGGCT	TTACAGGTGG	CAAATCCTA	GATCCTTCCA	TGGGAACAGG
Consensus	*****	*****	*****	*****	*****
	2151				2200
msa31161.2{327dNt_2603}	GAATTTCTTT	GCGGCTATGC	CAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327d_18RS21}	GAATTTCTTT	GCGGCTATGC	CAAACACTT	AAGAGAAAAG	AGTGAGTTGT
msa31161.2{327dNT_H36B}	GAATTTCTTT	GCGGCTATGC	CAAACACTT	AAGAGAAAAG	AGTGAGTTGT
Consensus	*****	*****	*****	*****	*****
	2201				2250
msa31161.2{327dNt_2603}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327d_18RS21}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
msa31161.2{327dNT_H36B}	ATGGCGTAGA	GTTAGATACT	ATTACAGGAG	CTATTGCCAA	ACACCTTCAT
Consensus	*****	*****	*****	*****	*****
	2251				2300
msa31161.2{327dNt_2603}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327d_18RS21}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
msa31161.2{327dNT_H36B}	CCCAATAGTC	ATATTGAAAT	TAAGGGATTT	GAGACGGTGG	CTTTTAACGA
Consensus	*****	*****	*****	*****	*****
	2301				2350
msa31161.2{327dNt_2603}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327d_18RS21}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
msa31161.2{327dNT_H36B}	CAATAGTTTT	GATTTGGTGA	TTTCAAATGT	GCCCTTTGCC	AATATACGAA
Consensus	*****	*****	*****	*****	*****
	2351				2400
msa31161.2{327dNt_2603}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327d_18RS21}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
msa31161.2{327dNT_H36B}	TTGCGGATAA	TAGGTACGAT	AGGCCTTACA	TGATTCATGA	CTACTTTGTC
Consensus	*****	*****	*****	*****	*****
	2401				2450
msa31161.2{327dNt_2603}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327d_18RS21}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
msa31161.2{327dNT_H36B}	AAAAAGTCAC	TTGATTTGCT	TCATGATGGT	GGACAAGTAG	CGATTATCTC
Consensus	*****	*****	*****	*****	*****
	2451				2500
msa31161.2{327dNt_2603}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327d_18RS21}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
msa31161.2{327dNT_H36B}	TTCCACAGGA	ACTATGGATA	AGCGAACAGA	AAACATCTTA	CAAGATATTC
Consensus	*****	*****	*****	*****	*****
	2501				2550
msa31161.2{327dNt_2603}	GTGAGACAAC	TGAATTTCTT	GTTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327d_18RS21}	GTGAGACAAC	TGAATTTCTT	GTTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
msa31161.2{327dNT_H36B}	GTGAGACAAC	TGAATTTCTT	GTTGGGGTTC	GACTGCCTGA	CTCTGCCTTT
Consensus	*****	*****	*****	*****	*****
	2551				2600
msa31161.2{327dNt_2603}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327d_18RS21}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
msa31161.2{327dNT_H36B}	AAGGCCATTG	CAGGAACGAG	TGTCACAACG	GATATGTTAT	TCITCCAGAA
Consensus	*****	*****	*****	*****	*****
	2601				2650
msa31161.2{327dNt_2603}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327d_18RS21}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
msa31161.2{327dNT_H36B}	ACACTTAGAC	AAGGGATATG	TGGCAGACGA	TTTAGCCTTT	TCAGGTTCCA
Consensus	*****	*****	*****	*****	*****
	2651				2700
msa31161.2{327dNt_2603}	TTTCGCTATGA	CAAGGATAGT	CGCATTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327d_18RS21}	TTTCGCTATGA	CAAGGATAGT	CGCATTGGC	TCAATCCTTA	TTTTGATGGA
msa31161.2{327dNT_H36B}	TTTCGCTATGA	CAAGGATAGT	CGCATTGGC	TCAATCCTTA	TTTTGATGGA
Consensus	*****	*****	*****	*****	*****
	2701				2750
msa31161.2{327dNt_2603}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327d_18RS21}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
msa31161.2{327dNT_H36B}	GAATACAATA	GCCAGGTGCT	AGGAACCTAC	GAGGTCAGGA	ATTTTAACGG
Consensus	*****	*****	*****	*****	*****
	2751				2800
msa31161.2{327dNt_2603}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG
msa31161.2{327d_18RS21}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG

Table 70: Comparative Sequences relating to SAG 1280

msa31161.2{327dnt_H36B}	AGGAACACTT	TCTGTTAAGG	GGACTAGTGA	TGACTTGATT	GCAAGTGTG	
Consensus	*****	*****	*****	*****	*****	*****
	2801					2850
msa31161.2{327dnt_2603}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG	
msa31161.2{327d_18RS21}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG	
msa31161.2{327dnt_H36B}	AAACAGCTCT	AAATCACGTT	AAGGCCCAA	GAGAGATTGA	TAGAAATGAG	
Consensus	*****	*****	*****	*****	*****	*****
	2851					2900
msa31161.2{327dnt_2603}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT	
msa31161.2{327d_18RS21}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT	
msa31161.2{327dnt_H36B}	GTCATCATT	ACCCAGATGT	GTTGACCAA	CAAGTCAATG	ATACCTCCAT	
Consensus	*****	*****	*****	*****	*****	*****
	2901					2950
msa31161.2{327dnt_2603}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG	
msa31161.2{327d_18RS21}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG	
msa31161.2{327dnt_H36B}	TCCAGCTGAA	ATGAGGGAAA	ATCTAGGTCA	GTACAGTTT	GGTTATCAGG	
Consensus	*****	*****	*****	*****	*****	*****
	2951					3000
msa31161.2{327dnt_2603}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG	
msa31161.2{327d_18RS21}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG	
msa31161.2{327dnt_H36B}	GGTCTACAGT	TTACTATCGA	GATAACAAAG	GCATTTCGAGT	CGGAACCAAG	
Consensus	*****	*****	*****	*****	*****	*****
	3001					3033
msa31161.2{327dnt_2603}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG		
msa31161.2{327d_18RS21}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG		
msa31161.2{327dnt_H36B}	ACGGAAGAAA	TCAGTTACTA	TGTCGATGAA	GAG		
Consensus	*****	*****	*****	***		

SEQ ID. NO. 7004

STRAIN H36B frame: 1

GGKMNQEVLLQMMRATI PRDRALLEAFLLYQAEHFDEEWDLSLIHQFMTNRQEIINKSVQVLF
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSLQKLDKLSPEKNLVI E VALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVRVANNLADRI SRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSVHQAI SFREEGSLVIASLDVDLSQLDVQIGKTSHLPA YEELSRLR
KFEILLTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLXIXLSQDFDPRVGI LLXAGRXRLKNADLASLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAFHLHQELSREDAEQFEKDK
GNQPDLLTRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
DARLNGLIRIELVNDPFSDI IEQNPLVYVRTWEEVSQALHQPKAEPQTELEEADQELNLF
FLEEEPVQSIGLEPPDSENGHNDTDL EETDNQIPEEEVETIPEI PVTDIFYFPEDLTD
YPKTARDKVETNI VAI RLVKNLEVEHRNASPSEQELLAKYVWGGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMSGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPPA
NIRIADNRYDRPYMIHDFYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPHYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLT
QVNDTSI PAEMRENLGQYSFGYQGSTVYVYRDNKGI RVGKTKEEISYYVDEE

SEQ ID. NO. 7005

STRAIN 18RS21 frame: 1

GGKMNQEVLLQMMRATI PRDRALLEAFLLYQAEHFDEEWDLSLIHQFMTNRQEIINKSVQVLF
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSLQKLDKLSPEKNLVI E VALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVRVANNLADRI SRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSVHQAI SFREEGSLVIASLDVDLSQLDVQIGKTSHLPA YEELSRLR
KFEILLTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLQDFDPRVGI LLDAAGFRLLKNADLALLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAFHLHQELSREDAEQFEKDK
GNQPDLLTRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS
DARLNGLIRIELVNDPFSDI IEQNPLVYVRTWEEVSQALHQPKAEPQTELEEADQELNLF
FLEEEPVQSIGLEPPDSENGHNDTDL EETDNQIPEEEVETIPEI PVTDIFYFPEDLTD
YPKTARDKVETNI VAI RLVKNLEVEHRNASPSEQELLAKYVWGGLANEFFDDYNPKFSK
EREELKSLVTDKEYSDMKQSSLTAYYTDPSLIRQMWDKLERDGTGGKILDPMSGTGNFF
AAMPKHLREKSELYGVELDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVPPA
NIRIADNRYDRPYMIHDFYFVKKSLDLLHDGGQVAI ISSTGTMDKRTENILQDIRETTEFL
GGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNPHYFDG
EYNSQVLGTYEVRNFGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVI INPDVLT
QVNDTSI PAEMRENLGQYSFGYQGSTVYVYRDNKGI RVGKTKEEISYYVDEE

SEQ ID. NO. 7006

STRAIN 2603 frame: 1

GGKMNQEVLLQMMRATI PRDRALLEAFLLYQAEHFDEEWDLSLIHQFMTNRQEIINKSVQVLF
HFETDVSAFVQASPYDTAHDLLTYTQVFGQSLQKLDKLSPEKNLVI E VALFNLATRFQ
LLDSNGHYQTISPDSLLQKSRGANLVNVRVANNLADRI SRDIEQFLTYEPELETRADE
TVLENEETVDEHKTSVHQAI SFREEGSLVIASLDVDLSQLDVQIGKTSHLPA YEELSRLR
KFEILLTYFDQIRNERSKVPSFRRGDFDTEMEMTPVFDGEEELLTYLEADGSPYELKRTLT
VEEKELEKIGQAIRIENQEKLTQLGIDLQDFDPRVGI LLDAAGFRLLKNADLALLGGYP
KASVTQLALATELLQMGLSHEKVEFFFGSLSIEELRQVAYAFHLHQELSREDAEQFEKDK
GNQPDLLTRDWKSKLEKAEGKEVVDEEFAENPLVQRVLDTYPLGSLVSYKGQDFEVMSVS

Table 70: Comparative Sequences relating to SAG 1280

DARLNGLIRIELVNDFSDII EQNPVLYVRTWEEVSQALHQPKEPQTELEEBADQELNLFSLFLEEEpVQSIGLLEPDDSENGHNDTDLLEETDNQIPBEEVETIPEIPVTDYFPPEDLTDYFKTARDKVTETNIVARLVKNLVEVHRNASPSEQBLLAKYVWGGLANEFFDDYNPKFASKEREELKSLVTDKEYSDMKQSSLTAYTDPISLRQMWKLERDGFTEGKILDDPSMGTGNFFAAMPKHLREKSELYGVLEDTITGAI AKHLHPNSHIEIKGFETVAFNDNSFDLVI SNVFFANIRIADNRYDRPYMIHDYFVKKSLDLLHDGGQVAIISSTGTMDKRTENILQDIRETTEFLGGVRLPDSAFKAIAGTSVTTDMLFFQKHLDKGYVADDLAFSGSIRYDKDSRIWLNYPYFDGEYNSQVLGTYEVRNFNGGTL SVKGTSDDLIASVETALNHVKAPREIDRNEVINPDLVTKQVNDTSIPAE MRENLGQYSPGYQGSTVYRDNKGI RVTGKTEEISYYVDEE

PRETTY of: /biotmp/msa23816.2{*} June 20, 2002 11:04 ..

msa23816.2{327dnt_H36B} 1 50
msa23816.2{327dnt_2603} gGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEHFDEEWD SLIHQFMNTR
msa23816.2{327d_18RS21} xGKMNQEVLL QMMRATIPRD RALLEAFLLY QAEHFDEEWD SLIHQFMNTR
Consensus -***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 51 100
msa23816.2{327dnt_2603} QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS
msa23816.2{327d_18RS21} QEINKSVQVL HFETDVSAFV QASPYDTAHD LLTYTQVFGQ SGLQKLDKLS
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 101 150
msa23816.2{327dnt_2603} PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVVYR
msa23816.2{327d_18RS21} PSEKNLVIEV ALFNLATRFQ LLDSNGHYQT ISPDSLLQKS RANLVNVVYR
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 151 200
msa23816.2{327dnt_2603} VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI
msa23816.2{327d_18RS21} VANNLADRIS RDIEQFLITY EPELETRADE TVLENEETVD EHKTSVHQAI
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 201 250
msa23816.2{327dnt_2603} SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSRR KFEILTYFDQ
msa23816.2{327d_18RS21} SFREEGSLVI ASLDVDLSQL DVQIGKTSHL PAYEELSRR KFEILTYFDQ
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 251 300
msa23816.2{327dnt_2603} IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT
msa23816.2{327d_18RS21} IRNERSKVPS FRRGDFDTEM EMTPVFDGEE LLTYLEADGS PYELKRTLIT
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 301 350
msa23816.2{327dnt_2603} VEEKELEKIG QAIRIENQEK LTQLxIxLSQ FDPDRVGILL xAAGRxRLxN
msa23816.2{327d_18RS21} VEEKELEKIG QAIRIENQEK LTQLgIdLSQ FDPDRVGILL dAAGRfRLkN
Consensus ***** ***** *-_*_*_* ***** -_*_*_*_*

msa23816.2{327dnt_H36B} 351 400
msa23816.2{327dnt_2603} ADLALGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA
msa23816.2{327d_18RS21} ADLALGGYP KASVTQLALA TELLQMGLSH EKVEFFFGSQ LSIEELRQVA
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 401 450
msa23816.2{327dnt_2603} YAFLhQELSR EDAAQFEKDK GNQPDLLTRD WSKLEKAEG KEVVDEEFAE
msa23816.2{327d_18RS21} YAFLhQELSR EDAAQFEKDK GNQPDLLTRD WSKLEKAEG KEVVDEEFAE
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 451 500
msa23816.2{327dnt_2603} NPLVQRVLDY YPLGSLVSYK QGDFEVMSVS DARLNGLIRI ELVNDFSDII
msa23816.2{327d_18RS21} NPLVQRVLDY YPLGSLVSYK QGDFEVMSVS DARLNGLIRI ELVNDFSDII
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 501 550
msa23816.2{327dnt_2603} EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSLFLEEEpVQSI
msa23816.2{327d_18RS21} EQNPVLYVRT WEEVSQALHQ PKAEPQTELE EADQELNLFSLFLEEEpVQSI
Consensus ***** ***** ***** ***** *****

msa23816.2{327dnt_H36B} 551 600
msa23816.2{327dnt_2603} GLEPDDSEN GHNDTDLLEET DNQIPBEEVV ETIPEIPVTD FYFPPEDLTDY
msa23816.2{327d_18RS21} GLEPDDSEN GHNDTDLLEET DNQIPBEEVV ETIPEIPVTD FYFPPEDLTDY
Consensus ***** ***** ***** ***** *****

Table 70: Comparative Sequences relating to SAG 1280

	601				650
msa23816.2{327dNT_H36B}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327dnt_2603}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
msa23816.2{327d_18RS21}	YPKTARDKVE	TNIVAIRLVK	NLEVEHRNAS	PSEQELLAKY	VGWGGLANEF
Consensus	*****	*****	*****	*****	*****
	651				700
msa23816.2{327dNT_H36B}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327dnt_2603}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
msa23816.2{327d_18RS21}	FDDYNPKFSK	EREELKSLVT	DKEYSDMKQS	SLTAYYTDPS	LIRQMWDKLE
Consensus	*****	*****	*****	*****	*****
	701				750
msa23816.2{327dNT_H36B}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327dnt_2603}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
msa23816.2{327d_18RS21}	RDGFTGGKIL	DPSMGTGNFF	AAMPKHLREK	SELYGVELDT	ITGAIAKHLH
Consensus	*****	*****	*****	*****	*****
	751				800
msa23816.2{327dNT_H36B}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327dnt_2603}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
msa23816.2{327d_18RS21}	PNSHIEIKGF	ETVAFNDNSF	DLVISNVPFA	NIRIADNRYD	RPYMIHDYFV
Consensus	*****	*****	*****	*****	*****
	801				850
msa23816.2{327dNT_H36B}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327dnt_2603}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
msa23816.2{327d_18RS21}	KKSLDLLHDG	GQVAIISSTG	TMDKRTENIL	QDIRETTEFL	GGVRLPDSAF
Consensus	*****	*****	*****	*****	*****
	851				900
msa23816.2{327dNT_H36B}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
msa23816.2{327dnt_2603}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
msa23816.2{327d_18RS21}	KAIAGTSVTT	DMLFFQKHL	KGYVADDLAF	SGSIRYDKDS	RIWLNPFYFDG
Consensus	*****	*****	*****	*****	*****
	901				950
msa23816.2{327dNT_H36B}	EYNSQVLGTY	EVRNFNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327dnt_2603}	EYNSQVLGTY	EVRNFNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
msa23816.2{327d_18RS21}	EYNSQVLGTY	EVRNFNGGTL	SVKGTSDDLI	ASVETALNHV	KAPREIDRNE
Consensus	*****	*****	*****	*****	*****
	951				1000
msa23816.2{327dNT_H36B}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTG
msa23816.2{327dnt_2603}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTG
msa23816.2{327d_18RS21}	VIINPDVLTK	QVNDTSIPAE	MRENLGQYSF	GYQGSTVYYR	DNKGIRVGTG
Consensus	*****	*****	*****	*****	*****
	1001	1011			
msa23816.2{327dNT_H36B}	TEEISYYVDE	E			
msa23816.2{327dnt_2603}	TEEISYYVDE	E			
msa23816.2{327d_18RS21}	TEEISYYVDE	E			
Consensus	*****	*			

Table 71: Comparative Sequences relating to SAG1333

SEQ ID NO. 7101
 STRAIN 2603
 ATGAAAAGAAAATATTTTGAAAAGTAGTGTCTTGGTTTGTAGTCGGTGGGACTTCTATT
 ATGTTCTCAAGCGTGTTCGCGGACCAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTT
 CATGGTGCACCTTGACAATCTGGAACAGCAAAATATGCCTGATGGAAAAGTTGCTAATGCT
 GGTACTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAACAACT
 AACCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGTTGGAGCAAGTCCAGCC
 AACTCTGGGCTTCTTCAAGATGAACCAACTGTCAAAAATTTAATGCAATGAATGTTGAG
 TATGGCACATTGGGTAACCATGAATTTGATGAAGGGTTGGCAGAATATAATCGTATCGTT
 ACTGGTAAAGCCCCGTCCAGATTCTAATATTAATAATATTACGAAATCATACCCACAT
 GAAGCTGCAAAAACAAGAAATTTAGTGGCAAAATTTATTGATAAAGTTAAACAAAACAAAT
 CCTTACAATTTGAAGCCTTACGCTATTAAAAATATTCCTGTAATAACAAAAGTGTGAAC
 GTTGGCTTTATCGGGATTGTCAACCAAGACATCCCAACCTTGTCTTACGTAAAAATTAT
 GAACAATATGAATTTTAGATGAAGCTGAAACAATCGTTAANTACGCCAAAGAAATTAACA
 GCTAAAAATGTCAAAGCTATTGTAGTTCTCGCACATGTACCTGCAACAAGTAAAAATGAT
 ATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTGAAAAAT
 AGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACAAATGGTCTTGTGGTAAA
 ACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGTGATGTACGTGGTGTCTTA
 GATACTGATACACAAGATTTCAATTGAGACCCCTTCAAGCTAAAGTAATTCAGTTGCTCCT
 GGTAAAAAACAGGTTAGTCCCGATATTCAAGCCATTGTTGACCAAGCTAATACATCTGTT
 AAACAAGTAAACAGAAAGTAAATTTGGTACTGCGGAGTAAAGTGTATGATTACGCGTTCT
 GTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCACTAGCAATT
 GCTCGAAAAAGCTGGCCAGATATCGATTTGCCATGACAAATAATGGTGGCATTTCGTCT
 GACTTACTCATCAACCCAGATGGAAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCT
 TTTGGTAAATCTTACAAGTCGTGAAATTAATGTTAGAGATCTTTATAAAGCACTCAAC
 GAACAATACGACCAAAAACAATAATTTCTTCTTCAATAGCTGGTCTGCGATACACTTAC
 ACAGATAATAAAGAGGGCGGGAAGAAACACCATTTAAAGTTGTAAAAGCTTATAAATCA
 AATGGTGGGAAATCAATCTGATGCAAAATACAAATTAGTTATCAATGACTTTTTATTTC
 GGTGGTGGTGTGGCTTTGGCAAGCTTCAGAAATGCCAAACTCTTAGGAGCCATTAACCCC
 GATACAGAGGTTATTATGGCTTATCACTGATTTAGAAAAGCTGGTAAAAAAGTGGAGC
 GTTCCAATAATAAACCTAAATCTATGTCACTATGAAGATGGTTAATGAAACTATTACA
 CAAAATGATGGTACACATAGCATTATTAAGAAACTTTATTTAGATCGACAAGGAAATATT
 GTAGCACAAAGAGATTGTATCAGACACTTTAAACCAAAACAAAATCAAAATCTACAAAATC
 AACCCCTGTAACCTACAATTCACAAAACAATAACCAAACTTTACAGCTATTAAACCCATG
 AGAAATTTATGGCAACCATCAACTCCACTACTGTAATAATCAAAACAATTACCAAAAACA
 AACTCTGAATATGGACAATCACTCTTATGTCTGTCTTGGTGGTGGACTTATAGGAATT
 GCTTTAAATACAAAAGAAAAACATATGAAA

SEQ ID NO. 7102
 STRAIN 090
 AAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACCTTGAC
 AATACTGGAACAGCAAAATATGCCTGACGGAAGGTTACTAATGCTGGCAC
 TGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAC
 AAATAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGTATGGTT
 GGAGCAAGTCCAGCTAACTCAGGCTTCTTCAAGATGAACCAACCGTTAA
 AACATTTAATGAATGAATGTTGAGTATGGCATTAGGTTAACCATGAAT
 TTGATGAAGGTTTGGCAGAAATCAATCGTATCGTTACTGGAAAGGCCCT
 GCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGAAGC
 TGCAAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAAACAAAC
 AAATCCCTTACAATTTGAAAACCTTACGCTATTAAAAATATTCCTGTAAT
 AACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAAGCATCCC
 AAACCTTGTCTTACGTAATAAATTTATGAACAATATGAATTTTATGATGAAG
 CTGAAAACAATCGTTAATAACGCAAGAAATTAACAAGCTAAAAATGTCAAG
 GCTATTGTAGTCTTGTCTCATGTACTCTGCAACCAAGCAAGGATGATATTGC
 TGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCTG
 AAAATAGCTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAAT
 GGTCTTGTGGTAAAACCTCGCATTGTACAAGCGCTCTCTCAAGGAAAAGC
 CTATGCTGACCGTACGTTGGTGTCTTATGATACGATACACAAGATTTCAATG
 AAACCCCTTACGTAAGTAGTTGAGTTGCTCCTGGTAAAAAAGCAGGT
 AGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAACA
 AGTAAACAGAGCTAAAATTTGTTACTGCGGAGGTAAGTGGCATGATTACGC
 GTTCTGTTGATCAAGATAATGTTAGTCCAGTAGGCAGCCTCATCACAGAG
 GCTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATTTTGGCCAT
 GACAAATAATGGTGGCATTCTGTGCTGACTTACTCATCAACCCAGATGGAA
 CAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAAATATCTTA
 CAAGTCTGCAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAACA
 ATACGACCAAAAACAATAATTTCTTCTTCAAAATAGCTGGTCTGCGATACA
 CTTACACAGATAATAAAGAGGGCGGAGAAGAAACACCATTTAAAGTTGTA
 AAAGCTTATAAATCAATGGTGAAGAAATCAATCCTGATGCAAAAATACAA
 ATTAGTTATCAATGACTTTTTATTTCGGTGGTGGTGGTGGCTTTGCAAGCT
 TCAGAAAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGTTATT
 ATGGCTTATCACTGATTTAGAAAAGCTGGTAAAAAAGTGGAGCTTCC
 AAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAACTA
 TTACACAAAATGATGGTACACATAGCATTATTAAGAAACTTTATTTAGAT
 CGACAAGGAAATTTGTAGCACAAAGAGATTGTATCAGACACTTTAAACCA
 AACAAAATCAAAATCTACAAAATCAACCCCTGTAACCTACAATTCACAAA
 AACAAATACCAATTTACAGCTATTAAACCTATGAGAAATTTAGGCAAA
 CCATCAACTCCACTACTGTAATAATCAAAACA

SEQ ID NO. 7103
 STRAIN A909
 GCGTCAATGACTTTTCATGGTGCCTTACCAATCTGGAACAGCAAAATATG
 CCTGACGGAAGGTTACTAATGCTGGCAGTCTGCTCAATTAGATGCTTA

Table 71: Comparative Sequences relating to SAG1333

TATGGATGATGCTCAAAAAGATTTCAAACAACTAACCCCTAATGGTGAAA
GCATTAGAGTTCAAGCTGGTGATATGGTTGGAGCAAGTCCAGCTAACTCA
GGGCTTCTTCAAGATGAACCAACCGTTAAAAACATTTAATGCAATGAATGT
TGAGTATGGCACATTAGGTAACCATGAAATTTGATGAAGGTTTGGCAGAAT
ACAATCGTATCGTTACTGGAAGGGCCCTGCTCCaGatTCTAATAATAAA
AATATACGAAATCATACCCACAGGCTGCAAAACAAGAAATTTAGT
GGCAAACGTTATGATAAAGTTAACAAACAATCCCTTACAATGGAAAC
CTTACACTATTAAAAATATTCCTGTAAATAACAAAAGTGTGAACGTTGGC
TTTATCGGAATCGTTACCAAAGACATCCCAAACCTTGTCTTACGTAAAAA
TTATGAACAATATGAATTTTATAGATGAAGCTGAAACAATCGTTAAATACG
CCAAAGAATTACAGCTAAAAATGTCAAGCTATTTGTAGTCTTGTCTCAT
GTACTGCAACAAGCAAGGATGATATTTGCTGAAGGTGAAGCAGCAGAAAT
GATGAAAAAAGTCAATCAACTCTTCCCTGAAAAATAGCGTAGATATTTGCT
TTGCTGGACACAATCATCAATATACAAATGGTCTTGTGTTGTTAAACCTCGT
ATTGTACAAGCGCTCTCTCAAGGAAAAGCCTATGTGTATGATCGTGGTGT
CCTAGATACTGATACACAGATTTCAATTGAAACCCCTTACAGCTAAAGTAA
TTGCAAGTTGCTCTTGGTAAAAAAGAGGTAGTGGCCGATATTCAAGCCATT
GTTGACCAAGCTAATACTATCGTTAAACAAGTAACAGAAGCTAAAAATGG
TACTGCCAGGTAAGTGGCATGATTACGCGTTCTGTTGATCAAGATAATG
TTAGTCCGGTAGGCAGCCTCATCACAGAGGCTCAACTAGCAATTTGCTCGA
AAAAGCTGGCCAGATATCGATTTTGCCATGACAAATAATGGTGGCATTCG
TGCTGACTTACTCATCAAAACAGATGGAACAATCACCTGGGGAGCTGCAC
AAGCAGTTCAACCTTTTGGTAATATCTTACAAGTCCGTGAAATTAAGTGT
AGAGATCTTTATAAAGCACTCAACGAACAATACGACCAAAAACAAAATTT
CTTCTTCAAATAGCTGGTCTGCGATACACTTACACAGATAATAAAGAGG
GCGGGGAAGAAAACCACTTTAAAGTTGTAAGAGCTTATAAATCAAATGGT
GAGGAAATCAATCCTGATGCAAAATACAAATAGTTATCAATGACTTTTT
ATTCGGTGGTGGTGGTGGCTTTGCAAGCTTCAGAAATGCCAAACTCTAG
GAGCCATTAATCCGATACAGAGGTAATTTATGGCCTATATCACTGATTTA
GAAAAAGCTGGTAAAAAAGTGAAGCTTCCAAATAATAAACCTAAAATCTA
TGTCACTATGAAGATGGTTAATGAAACTATTAACAATAATGATGGTACAT
ATAGCATTATTAAGAACTTTATTTAGATCGACAAGGAAATATTGTAGCA
CAAGAGATTGTATCAGACACTTTAAACCAACAATAATAATAATAATAA
AATCAACCTGTAACTACAATTCAAAAAACAATTACACCAATTTACAG
CTATTAACCTATGAGAAATTTATGGCAAACCATCAAACTCCACTACTGTGA
AAATCAAAACA

SEQ ID NO. 7104

STRAIN H36B

CCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACCTG
ACAATACTGGAACAGCAAATATGCCTGACGGAAAAGTTACTAATGCTGGC
ACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
ACAAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGAATGG
TTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTT
AAAAATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGA
ATTTGATGAAGTTTGGCAGAATACAATCGTATCGTTACTGGAAAAGGCC
CTGCTCCAGATTCTAATATAAATAATATTACGAAATCATAACCCACAGAA
GCTGCAAAAACAGAAATTTGATGTCGCAACGTTATGATAAAGTTAACAA
ACAAATCCCTTACAATGGAAACCTTACACTATTAATAAATAATTTCTGTAA
ATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAGACATC
CCAAACCTTGTCTTACGTAATAAATATGAACAATATGAATTTTATAGATGA
AGCTGAAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTCA
AGGCTATTGTAGTCCCTGCTCATGTACTGCAACAAGCAAGGATGATATT
GCTGAAGGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTTCCC
TGAAAAATAGCGTAGATATTTGCTTTGCTGGACACAATCATCAATATACAA
ATGCTCTTGTGGTAAAACCTCGTATTTGATCAAGCGCTCTCTCAAGGAAA
GCCTATGCTGATGATACGTTGGTGGTCTTATAGATGATACACAGATTTAT
TGAACCCCTTCAAGTAAAGTAATTTGCAGTTGCTCTGGTAAAAAACAAG
GTAGTGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAA
CAAGTAACAGAAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTAC
GCGTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAG
AGGCTCAACTAGCAATGCTCGAAAAAGCTGGCCAGATATCGATTTTGGC
ATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAAACAGATGG
AACAACTCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATCT
TACAAGTCTGCGAAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGAA
CAATACGACCAAAAACAATAATTTCTTCTTCAAATAGCTGGTCTGCGATA
CACTTACACAGATAATAAAGAGGGCGGGGAAGAAACCAATTTAAAGTTG
TAAAAGCTTATAAATCAAATGGTGAAGAAATCAATCCTGATGCAAAATAC
AAATTAGTTATCAATGACTTTTATTTGCTGGTGGTGGTGGTGGTGGTGGT
CTTCAAGAAATGCCAAACTCTAGGAGCCATTAATCCGATACAGAGGAT
TTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCTT
CCAAATAATAAACCCTAAAATCTATGCTCACTATGAAGATGGTTAATGAAAC
TATTAACAATAAATGATGGTACATATAGCATTTATAAAGAACTTTATTTAG
ATCGACAAGGAAATATTGTAGCACAGAGATTGTTATCAGACACTTAAAC
CAAAACAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA
AAAACAATTACACCAATTTACAGCTATTAAACCTATGAGAAATTTGGCA
AACCATCAAACTCCACTACTTAAAATCAA

SEQ ID NO. 7105

STRAIN 18RS21

GACCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTT
ATGGTGCACCTGCAATACTGGAAACAGCAAATATGCCTGACGGAAAAGTT
AnTAATGCTGGCAGTCTGCTCAATTAGATGCTTATATGGATGATGCTCA

Table 71: Comparative Sequences relating to SAG1333

AAAAGATTTCAAACAACTAACCCCTAATGGTGAAAGCATTAGAGTTCAAG
 CTGGTGATATGGTTGGAGCAAGTCCAGCTAACCTCAGGGCTTCTTCAAGAT
 GAACCAACCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATT
 AGGTAACCATGAATTTGATGAAGTTTGGCAGAATACAATCGTATCGTTA
 CTGGAAAGGCCCCCTGCTCCAGATTCTAATATAAATAATATACGAAATCA
 TACCCACACGAAGCTGCAAAAACAGAAATTTAGTAGGCAAAACGTTATTGA
 TAAAGTTAAACAAACAAATCCCTTACAATTTGGAACCTTACACTATTAATA
 ATATTCCCTGTAATAACAAAGTGTGAACGTTGGCTTTATCGGAATCGTT
 ACCAAAGACATCCCAACCTTGTCTTACGTAAAAATTTATGAACATATGA
 ATTTTTAGATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATTACAAG
 CTAAAAATGTCAAGGCTATTTAGTCTTGTCTCATGTACCTGCAACAAGC
 AAGGATGATATGCTGAAGTGAAGCAGCAGAAATGATGAAAAAGTCAA
 TCAACTCTTCCCTGAAAATAGCGTAGATATTGTCTTTGCTGGACACAATC
 ATCAATATACAATGGTCTTGTGGTAAAACCTCGTATTGTACAAGCGCTC
 TCTCAAGGAAAAGCCTATGCTGATGATCGTGGTGTCTTAGATACTGATAC
 ACAAGATTTCATTGAAACCCCTTCAAGTAAAGTAAATGCGAGTTGCTCCTG
 GTAAAAAACAGGTTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAAT
 ACTATCGTTAAACAAGTACAGAAGCTAAAATTTGGTACTGCCGAGGTAAG
 TGGCATGATTACCGGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCA
 GCCTCATCACAGAGGCTCACTAGCAATTTGCTCGAAAAGCTGGCCAGAT
 ATCGATTTTGGCCATGACAAAATAATGGTGGCATTGCTGCTGACTTACTCAT
 CAAACCGATGGAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTT
 TTGGTAATATCTTACAAGTCTCGAAATTAAGTGGTAGAGATCTTTATAAA
 GCACCTCAACGAAACAATACGACCAAAAACAAAATTTCTTCTTCAAATAGC
 TGGTCTGCGATACACTTACACAGATAATAAGAGGGCGGGGAAGAAACAC
 CATTTAAAGTTGTAAGCTTATAAATCAAATGGTGAAGAAATCAATCTT
 GATGCAAAATACAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGA
 TGGCTTTGCAAGCTTCAAGAAATGCCAACTTCTTAGGAGCCATTAATCCCG
 ATACAGAGGATATTATGCGCTATATCACTGATTAGAAAAAGCTGGTAAA
 AAGTGGAGCGTTCCAATAATAAACCCTAAAATCTATGTCATATGAAGAT
 GGTAAATGAAACTATTACAAAAATGATGGTACATATAGCATTATTAAGA
 AACTTATTAGATCGACAAGGAAATATTGTAGCACAAGAGATTGTATCA
 GACTTTAAACCAACAAAATCAAATCTACAAAAATCAACCTGTAAAC
 TACAATTCACAAAAACAATTACACCAATTTACAGCTATTAAACCTATGA
 GAAATTTAGGCAAAACCTCAACTCCACTACTGTAATCAAAA

SEQ ID NO. 7106

STRAIN M732

ACCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAACTCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
 AACAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGATATG
 GTTGGAGCAAGTCCAGCTAACCTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAAATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATG
 AATTGATGAAGTTTGGCAGAATACAATCGTATCGTTACTGGAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATACGAAATCATACCCACACGA
 AGCTGCAAAACAAGAAATTTAGTGGCAACGTTATTGATAAAGTTAACAA
 AACAAATCCCTTACAATTTGAAACCTTACACTATTAAAAATATTCCTGTA
 AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
 CCCAAACCTTGTCTTACGTAATAATATGAAACAATATGAATTTTTAGATG
 AAGCTGAAACAATCGTTAAATACGCAAGAAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCTTGTCTCATGTACTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGTTGTTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTCTCTAGATACTGATACACAAGATTTCA
 TTGAAACCCCTTCAAGTAAATTTGCAAGTGTCTCTGGTAAAAAACA
 GGTAGTCCCGATATTCAAGCATTGTTGCAAGCTAATACTACTCGTTAA
 ACAAGTAAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATTTGCTCGAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAATAATGGTGGCATTGCTGCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGGAGCTGCACAAGCAGTTCAACCTTTGGTAATATC
 TTACAAGTCTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
 ACAATACGACCAAAAACAATAATTTCTTCTTCAAATAGCTGGTCTGCGAT
 ACCTTACACAGATAATAAGAGGGCGGGGAAGAAACACCAATTTAAAGTT
 GTAAAGCTTATAAATCAAATGGTGAAGAAATCAATCTGATGCAAAATA
 CAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTGGTGGCTTTGCAA
 GCTTCGAAATGCCAACTTCTAGGAGCCATTAATCCCGATACAGAGGTA
 TTTATGGCCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGGCAT
 TCCAAATAATAAACCTAAAATCTATGTCATATGAAGATGGTTAATGAAA
 CTATTACAAAAATGATGGTACATATAGCAATTTAAGAAACTTTATTTA
 GATCGACAAGGAAATTTGTAAGCACAAGAGATTGTATCAGACTTTAA
 CCAAACAAAATCAAATCTACAAAAATCAACCTGTAACTACAAATTCACA
 AAAAAAATTACACCAATTTACAGCTATTAAACCTATGAGAAATTTAGG
 AACCATCAAACCTCAACTGTAATCAAAA

SEQ ID NO. 7107

STRAIN COHI

ACCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTTCATGGTGCACTT
 GACAACTCTGGAACAGCAAAATATGCTGACGGAAGTTACTAATGCTGG
 CACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCA
 AACAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGATATG

Table 71: Comparative Sequences relating to SAG1333

GTTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGT
 TAAAACTTTAATGCAATGAAATGTTGAGTATGGCACATAGGTAACCATG
 AATTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCC
 CCTGCTCCAGATTCTAATATAAATAATATTACGAAATCATACCCACACGA
 AGCTGCAAAAACAAGAAATGTAGTGGCAAACGTTATTGATAAAGTTAAACA
 AACAATCCCTTACAATGGAAACCTTACACTATTAAAAATATTCTGTGA
 AATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACAT
 CCCAAACCTTGTCTTACGTAATAAATATGAACAATATGAATTTTGTAGATG
 AAGCTGAAAACAATCGTTAAATACGCCAAAGAATTACAAGCTAAAAATGTC
 AAGGCTATTGTAGTCCCTTGTCTCATGTACTGCAACAAGCAAGGATGATAT
 TGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCC
 CTGAAAAATAGCGTAGATATTGTCTTTGTCTGGACACAATCATCAATATACA
 AATGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAA
 AGCCTATGCTGATGTACGTGGTGTCTAGATACTGATACACAAGATTCA
 TTGAAACCCCTTCAAGTAAAGTAATGCAAGTGTCTCTGGTAAAAAACA
 GGTAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAA
 ACAAGTAAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATGATTA
 CGCGTTCTGTGGTCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACA
 GAGGCTCAACTAGCAATGCTCGAAAAGCTGGCCAGATATCGATTTTGC
 CATGACAAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATG
 GAACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAATATC
 TTACAAGTCTGTCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCAACGA
 ACAATACGACCAAAAACAATAATTTCTTCTTCAANTAGCTGGTCTGCGAT
 ACACCTTACACAGATAATAAGAGGGCGGGGAAGAAACACCATTAAAGTT
 GTAAAGCTTTATAAATCAAAATGGTGAAGAAATCAATCTGATGCAAAATA
 CAAATTAGTTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGCTTTGCAA
 GCTTCAGAAATGCCAACTCTTAGGAGCCATTATCCGATACAGAGGTA
 TTTATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGGAGCAT
 TCCAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTTAATGAAA
 CTATTACACAAAATGATGGTACATATAGCATTATTAAGAAAATTTATTTA
 GATCGACAAGGAAATATGTAGCACAAAGAGATTGTATCAGACACTTTAA
 CCAAACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCA
 AAAAAAATTAACCAATTTACAGCTATTAAACCTATGAGAAATATGGC
 AAACCATCAAACTCCACTACTGTAATAACAA

SEQ ID NO. 7108
STRAIN M781

CAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGCACCTTGA
 CAATACTGGAAACAGCAATATGCCTGACGGAAAAGTTACTAATGCTGGCA
 CTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAA
 CAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGGATATGGT
 TGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTA
 AAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAACCATGAA
 TTTGATGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCC
 TGCTCCAGATTCTAATAATAAATAATATTACGAAATCATACCCACACGAA
 CTGCAAAAACAAGAAATGTAGTGGCAAACGTTATTTGATAAAGTTAACA
 CAAATCCCTTACAATTTGAAACCTTACACTATTAAAAATATTTCTGTAAA
 TAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGCATCC
 CAAACCTTGTCTTACGTAATAAATTAAGAACAATATGAATTTTGTAGATGA
 GCTGAAAACAATCGTTAATAACGCCAAAGAATTACAAGCTAAAAATGTCAA
 GGCTATTGTAGTCTTGTCTCATGTACTGCAACAAGCAAGGATGATATTG
 CTGAAGGTGAAGCAGCAGAAAATGATGAAAAAGTCAATCAACTCTTCCCT
 GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAA
 TGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
 CCTATGCTGATGTACGTGGTGTCTTAGATACTGATACACAAGATTTCAAT
 GAAACCCCTTCAAGTAAAGTAAATGCAAGTGTCTCTGGTAAAAAACAAG
 TAGTGGCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
 AAGTAACAGAAGCTAAAATGGTACTGCGGAGGTAAGTGGCATGATTACG
 CGTTCTGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGA
 GGCTCAACTAGCAATGCTCGAAAAGCTGGCCAGATATCGATTTTGGCCA
 TGACAAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGA
 ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAAATATCTT
 ACAAGTCTGCAAAATTAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 AATACGACCAAAAACAATAATTTCTTCTTCAAATAGCTGGTCTGCGGATAC
 ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCATTAAAGTTGT
 AAAAGCTTATAAATCAAAATGGTGAAGAAATCAATCTGATGCAAAATACA
 AATTAGTTATCAATGACTTTTATTCTGGTGGTGGTGGTGGTGGTGGTGGT
 TTCAGAAAATGCCAAACTTCTAGGAGCCATTATCCCGATACAGAGTATT
 TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAGTGGAGCATTC
 CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTAAATGAAACT
 ATTTACAAAAATGATGGTACATATAGCATTATTAAGAAAATTTATTTAGA
 TCGACAAGGAAAATTTAGTACACAAGAGATTGTATCAGACACTTTAAACC
 AAACAAAATCAAAATCTACAAAATCAACCTGTAACTACAATTCAAAA
 AAACAATTAACCAATTTACAGCTATTAAACCTATGAGAAATATGGCAA
 ACCATCAAACTCCACTACTGTAATAACAA

SEQ ID NO. 7109
STRAIN CJB110

GACCAAGTCCGGTGTCCAAGTTATAGGCGTCAATGACTTTCATGGTGC
 ACTTGACAATACTGGAAACAGCAATATGCCTGACGGAAAAGTTACTAATG
 CTGGCACTGCTGCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGAT
 TTCAAAACAACTAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTGA
 TATGGTGGAGCAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAA

Table 71: Comparative Sequences relating to SAG1333

CCGTTAAACATTTAATGCAATGAATGTTGAGTATGGCACATTAGGTAAC
CATGAATTTGATGAAGTGGTGGCAGAATACAATCGTATCGTTACTGGAAA
GGCCCTGCTCCAGATTCTAATATAAATAAATACGAAATCATAACCAC
ACGAAGCTGCAAAACAAGAAATGTTAGTGGCAACCGTTATGATAAAGTT
AACAAACAAATCCCTTACAATGGAAACCTTACGCTATTAATAATATCC
TGTAAATAACAAAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAA
ACATCCCAACCTTGTCTTACGTAATAAATATGAACAATATGAATTTTFA
GATGAAGCTGAAACAATCGTTAAATACGCCAAAGAATACAAAGCTAAAA
TGTCAAGGCTATGTAGTCTTGTCTCATGTACCTGCAACAAGCAAGGATG
ATATTGCTGAAGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTC
TTCCCTGAAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATA
TACAAATGGTCTTGTGGTAAAACCTCGCATTGTACAAGCGCTCTCTCAAG
GAAAAGCCTATGTCTGACGTACGTGGTGTCTAGATACTGATACAAAGAT
TTCATTGAAACCCCTTACGCTAAAGTAGTTGCAAGTTGCTCTCTGGTAAAA
AACAGGTAGTGGCGATATTCAAGCCATTGTGACCAAGCTAATATCTATCG
TTAAACAAGTAAACAGAAGCTAAAAATGGTACTGCCGAGGTAAGTGGCATG
ATTACCGCTTCTGTGATCAAGATAATGTTAGTCCAGTAGGCAGCCCTCAT
CACAGAGCTCAACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGATT
TTGCCATGACAAATAATGGTGGCATTCTGTCTGACTTACTCATCAAACCA
GATGGAAACAATCACTGGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAA
TATCTTACAAGTGTGCGAAATTAAGTGGTAGAGATCTTTATAAAGCACTCA
ACGAACAATACGACCAAAAAAATAATTTCTTCTCAATAGCTGGTCTG
CGATACCTTACACAGATAATAAAGAGGGCGGAGAAGAAACCACTTTAA
AGTTGTAAAAGCTTATAAATAAATAAATGGTGAAGAAATCAATCCTGATGCAA
AATACAAATTAGTTATCAATGACTTTTATTTCGGTGGTGGTATGGCTTT
GCAAGCTTACAGAAATGCCAACTTCTAGGAGCATTAAATCCGATACAGA
GGTATTTATGGCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGA
GCGTTCAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
GAACTATTTACACAAATGATGGTACACATAGCATTATTAAGAACTTTA
TTTAGATCGACAGGAAATATTTAGCACAAGAGATTGTATCAGACACTT
TAAACCAACAAATCAAAATCTACAAATAAATAAATAAATAAATAAATAAATAA
CACAAAAACAATTACACCAATTTACAGCTATTACCCCTATGAGAAATTA
TGGCAACCATCAAACTCACTACTGTAATAATCA

SEQ ID NO. 7110

STRAIN 1169NT

CAAGTCGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACCTTGA
CAATACTGGAACAGCAAAATATGCCTGATGGAAAAGTTGCTAATGCTGGTA
CTGCTGCTCAATTAGATGCTTATATGGATGACGCTCAAAAAGATTTCAAA
CAAACTAACCCCTAATGGTGAAGCATTAGGGTTCAAGCAGGCGATATGGT
TGGAGCAAGTCCAGCCAACTCTGGCTTCTTCAAGATGAACCAACTGTCA
AAAATTTAATGCAATGAATGTTGAGTATGGCACATTGGGTAACCATGAA
TTTGATGAAGGGTTGGCAGAAATATAATCGTATCGTTACTGGTAAAGCCCC
TGCTCCAGATTCTAATATAAATAAATAAATAAATAAATAAATAAATAAATAA
CTGCAAAACAAGAAATGTTAGTGGCAAAATGTTATGATAAAGTTAACAAA
CAAATTCCTTACAATGGAAAGCCTTACGCTATTAAAAATAATCTCTGTAAA
TAAACAAAGTGTGAACGTTGGCTTTATCGGGATTGTCAACAAAGACATCC
CAACCTTGTCTTACGTAATAAATAAATAAATAAATAAATAAATAAATAAATAA
GCTGAAACAATCGTTAAATAACGCAAAAGAAATACAAGCTAAAAATGTCAA
AGCTATTGTAGTCTCGCACATGTACCTGCAACAAGTAAAAATGATATTG
CTGAAGGGTGAAGCAGCAGAAATGATGAAAAAGTCAATCAACTCTTCCCT
GAAAATAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAA
TGGTCTTGTGGTAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAG
CCTATGCTGATGTACGTTGGTCTCTTAGATACTGATACACAAGATTTCATT
GAGACCCCTTACGCTAAAGTAATTGCAGTTGCTCTGGTAAAAAACAAGG
TAGTGGCCGATATTCAAGCCATTGTTGACCAAGCTAATACTATCGTTAAAC
AAGTAACAGAAGCTAAAATGGTACTGCCGAGGTAAGTGTATGATTACG
CGTTCTGTTGATCAAGATAATGTTAGTCCGCTAGGCAGCCCTCATCACAGA
GGCTCAACTAGCAATGCTCGAAAAAGCTGGCCAGATATCGATTTTGCCA
TGACAAATAAATGGTGGCATTCTGTCTGACTTACTCATCAAACAGATGGA
ACAATCACCTGGGAGCTGCACAAGCAGTTCAACCTTTTGGTAAATATCTT
ACAAGTCTGCGAAATTAATGGTAGAGATCTTTATAAAGCACTCAACGAAC
AATACGACCAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
ACTTACACAGATAATAAAGAGGGCGGGGAAGAAACACCAATTTAAAGTGT
AAAAGCTTATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA
AATTAGTTATCAATGACTTTTATTTCGGTGGTGGTATGGCTTTGCAAGC
TTCAGAAATGCCAAACTTCTAGGAGCCATTAAACCCGATACAGAGGTATT
TATGGCCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAAGCGTTC
CAAATAATAAACCTAAAATCTATGTCACTATGAAGATGGTAAATGAACT
ATTACACAAAATGATGGTACACATAGCATTATTAAGAACTTTATTTAGA
TCGACAAGGAAATATTTAGCACAAGAGATTGTATCAGACACTTTAAAC
AAACAAAATCAAAATCTACAAAAATCAACCCCTTAACTACAAATCACAAA
AAACAATTACCAATTTACAGCTATTAAACCCCTATGAGAAATATGGCAA
ACCATCAAACTCACTACTGTAATAATCAAA

SEQ ID NO. 7111

STRAIN JM9130013

CGGTGTCCAAGTTATAGGCGTCAATGACTTTTATGGTGCACCTTGACAATA
CTGGAACAGCAAAATATGCCTGACGGAAGTTACTAATGCTGGCACTGCT
GCTCAATTAGATGCTTATATGGATGATGCTCAAAAAGATTTCAAAACAAC
TAACCCCTAATGGTGAAGCATTAGAGTTCAAGCTGGTATGGTGGGAG
CAAGTCCAGCTAACTCAGGGCTTCTTCAAGATGAACCAACCGTTAAACCA
TTTAAATGCAATGAATGTTAGTATGGCACATTAGGTAACCATGAATTTGA

Table 71: Comparative Sequences relating to SAG1333

TGAAGGTTTGGCAGAATACAATCGTATCGTTACTGGAAAGGCCCTGCTC
CAGATTcTAATATAAATAATATTACGAAATCATACCCACAGGCTGCA
AAACAAGAAATTTAGTGGCAACCGTTATTGATAAAGTTAACAAAATAAT
CCCTTACAATTTGAAACCTTACACTATTAATAAATATTCTGTAAATAACA
AAAGTGTGAACGTTGGCTTTATCGGAATCGTTACCAAAGACATCCCAAAC
CTTGTCTTACGTAATAAATATGAACAATATGAATTTTTAGATGAAGCTGA
AACAAATCGTTAAATACGCCAAAGAATTACAAAGCTAAAAATGTCAAGGCTA
TTGTAGTCCCTTGTCTCATGTACCTGCAACAAGCAAGGATGATATTGCTGAA
GGTGAAGCAGCAGAAATGATGAAAAAAGTCAATCAACTCTCCCTGAAAA
TAGCGTAGATATTGTCTTTGCTGGACACAATCATCAATATACAAATGGTC
TTGTTGGTAAAACTCGTATTGTACAAGCGCTCTCTCAAGGAAAAGCCTAT
GCTGATGTACGTTGGTGTCTAGATACATGATACACAAGATTTCAATGAAAC
CCCTTCAGCTAAAGTAATGCAAGTTGCTCCTGGTAAAAAACAGGTAGTG
CCGATATTCAAGCCATTCTTGACCAAGCTAATACTATCGTTAAACAAGTA
ACAGAAGCTAAAAATGGTACTGCGGAGGTAAGTGGCATGATTACGCGTTC
TGTTGATCAAGATAATGTTAGTCCGGTAGGCAGCCTCATCACAGAGGCTC
AACTAGCAATTTGCTCGAAAAAGCTGGCCAGATATCGAATTTGCCATGACA
AATAATGGTGGCATTCGTGCTGACTACTCATCAAACCAGATGGAACAAT
CACCTGGGGAGCTGCACAAGCAAGTTCAACCTTTTGGTAATATCTTACAAG
TCGTGCAAAATTAATCGGTAGAGATCTTTATAAAGCACTCAACGAAACAATC
GACCAAAAAATAAATTTCTTCCTTCAAATAGCTGGTCTGCGATACACTTA
CACAGATAATAAAGAGGGCGGGGAAGAAACACCATTTAAAGTTGTAAAG
CTTATAAATCAAATGGTGGGAAATCAATCCTGATGCAAAATACAAATTA
GTTATCAATGACTTTTATTTCGGTGGTGGTGAAGGCTTTGCAAGCTTCAG
AAATGCCAAACTTCTAGGAGCCATTAATCCCGATACAGAGGATTTTATGG
CCTATATCACTGATTTAGAAAAAGCTGGTAAAAAAGTGAGCGTTCCAAAT
AATAAACCTAAAAATCTATGCTCACTATGAAGATGGTAAATGAAACTATTAC
ACAAATGATGGTACATATAGCATTATTGAGAAACTTTATTAGATCGAC
AAGGAAATATTGTAGCAACAAGAGATTGTATCAGACACTTTAAACCAAACA
AAATCAAAATCTACAAAATCAACCTGTAACTACAATTCACAAAAACA
ATTACACCAATTTACAGCTATTACCTATGAGAAATTTAGGCAACCAT
CAAATCCACTACTGTAAATCAAAA

PRETTY of: /biotmp/msa237456.2{*} May 14, 2003 03:20 ..

1 50
msa237456.2{328_1169NT}
msa237456.2{328_2603} atgaaaaaga aaattattht gaaaagttagt gtctctgggt tagtcgctgg
msa237456.2{328_18RS21}
msa237456.2{328_H36B}
msa237456.2{328_COH1}
msa237456.2{328_M732}
msa237456.2{328_M781}
msa237456.2{328_JM9130013}
msa237456.2{328_A909}
msa237456.2{328_090}
msa237456.2{328_CJB110}
Consensus *****

51 100
msa237456.2{328_1169NT}
msa237456.2{328_2603} gacttctatt atgttctcaa gcggtgtcgc gGACcaagtc ggtgtccaag
msa237456.2{328_18RS21}
msa237456.2{328_H36B}
msa237456.2{328_COH1}
msa237456.2{328_M732}
msa237456.2{328_M781}
msa237456.2{328_JM9130013}
msa237456.2{328_A909}
msa237456.2{328_090}
msa237456.2{328_CJB110}
Consensus *****

101 150
msa237456.2{328_1169NT}
msa237456.2{328_2603} ttatagGCGT CAATGACTTT CATGGTGCAC TTGACAATAC TGGAACAGCA
msa237456.2{328_18RS21}
msa237456.2{328_H36B}
msa237456.2{328_COH1}
msa237456.2{328_M732}
msa237456.2{328_M781}
msa237456.2{328_JM9130013}
msa237456.2{328_A909}
msa237456.2{328_090}
msa237456.2{328_CJB110}
Consensus *****

151 200
msa237456.2{328_1169NT}
msa237456.2{328_2603} AATATGCCTG AtGGAAAAGT TgcTAATGCT GGtACTGCTG CTCAATTAGA
msa237456.2{328_18RS21}
msa237456.2{328_H36B}
msa237456.2{328_COH1} AATATGCCTG AcGGAAAAGT TacTAATGCT GgCACTGCTG CTCAATTAGA
AATATGCCTG AcGGAAAAGT TacTAATGCT GgCACTGCTG CTCAATTAGA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_M732}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_M781}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_JM9130013}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_A909}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
msa237456.2{328_CJB110}	AATATGCCTG	AcGGAAAAGT	TacTAATGCT	GGcACTGCTG	CTCAATTAGA
Consensus	*****	*-*****	*-*****	*-*****	*****
msa237456.2{328_1169NT}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_2603}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_18RS21}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_H36B}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_COH1}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_M732}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_M781}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_JM9130013}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_A909}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_090}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
msa237456.2{328_CJB110}	TGCTTATATG	GATGAcGCTC	AAAAAGATT	CAAACAACT	AACCCTAATG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_2603}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_18RS21}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_H36B}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_COH1}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M732}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_M781}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_JM9130013}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_A909}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_090}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
msa237456.2{328_CJB110}	GTGAAAGCAT	TAGgGTTCAA	GcAGGcGATA	TGGTTGGAGC	AAGTCCAGCc
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AACTCtGGGC	TTCTTCAAGA	TGAACCAACT	GTCAAAAaT	TTAATGCAAT
msa237456.2{328_2603}	AACTCtGGGC	TTCTTCAAGA	TGAACCAACT	GTCAAAAaT	TTAATGCAAT
msa237456.2{328_18RS21}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_H36B}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_COH1}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_M732}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_M781}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_JM9130013}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_A909}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_090}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
msa237456.2{328_CJB110}	AACTCaGGGC	TTCTTCAAGA	TGAACCAAcC	GTTAAAAcaT	TTAATGCAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_2603}	GAATGTTGAG	TATGGCACAT	TgGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_18RS21}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_H36B}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_COH1}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_M732}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_M781}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_JM9130013}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_A909}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_090}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
msa237456.2{328_CJB110}	GAATGTTGAG	TATGGCACAT	TaGGTAACCA	TGAATTTGAT	GAAGGtTTGG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	CAGAATAtAA	TCGTATCGTT	ACTGGtAAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_2603}	CAGAATAtAA	TCGTATCGTT	ACTGGtAAAg	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_18RS21}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_H36B}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_COH1}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M732}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_M781}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_JM9130013}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_A909}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_090}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
msa237456.2{328_CJB110}	CAGAATAcAA	TCGTATCGTT	ACTGGaAAgG	CCCCTGCTCC	AGATTCTAAT
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ATtAAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_2603}	ATtAAATAATA	TTACGAAATC	ATACCCACat	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_18RS21}	ATaAAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_H36B}	ATaAAATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_COH1}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M732}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_M781}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_JM9130013}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_A909}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
msa237456.2{328_CJB110}	ATaATAATA	TTACGAAATC	ATACCCACac	GAAGCTGCAA	AACAAGAAAT
Consensus	***-*****	*****-***	*****-***	*****-***	*****-***
501					
msa237456.2{328_1169NT}	TGTAGTGGCA	AAtGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_2603}	TGTAGTGGCA	AAtGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_18RS21}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_H36B}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_COH1}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M732}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_M781}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_JM9130013}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_A909}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_090}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
msa237456.2{328_CJB110}	TGTAGTGGCA	AAcGTTATTG	ATAAAGTTAA	CAAACAAATc	CCTTACAATT
Consensus	*****-***	***-*****	*****-***	*****-***	*****-***
551					
msa237456.2{328_1169NT}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_2603}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_18RS21}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_H36B}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_COH1}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M732}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_M781}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_JM9130013}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_A909}	GGAAaCCTTA	CaCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_090}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
msa237456.2{328_CJB110}	GGAAaCCTTA	CgCTATTAAA	AATATTCCCTG	TAAATAACAA	AAGTGTGAAC
Consensus	****-*****	*-*****	*****-***	*****-***	*****-***
601					
msa237456.2{328_1169NT}	GTTGGCTTTA	TCGGgATtGT	cACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_2603}	GTTGGCTTTA	TCGGgATtGT	cACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_18RS21}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_H36B}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_COH1}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M732}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_M781}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_JM9130013}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_A909}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_090}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
msa237456.2{328_CJB110}	GTTGGCTTTA	TCGGaATcGT	tACCAAAGAC	ATCCCAAACC	TTGTCTTACG
Consensus	*****-***	****-***-***	-*****-***	*****-***	*****-***
651					
msa237456.2{328_1169NT}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_2603}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_18RS21}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_H36B}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_COH1}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M732}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_M781}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_JM9130013}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_A909}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_090}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
msa237456.2{328_CJB110}	TAAAAATTAT	GAACAATATG	AATTTTTAGA	TGAAGCTGAA	ACAATCGTTA
Consensus	*****-***	*****-***	*****-***	*****-***	*****-***
701					
msa237456.2{328_1169NT}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_2603}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTc
msa237456.2{328_18RS21}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_H36B}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_COH1}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_M732}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_M781}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_JM9130013}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_A909}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_090}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
msa237456.2{328_CJB110}	AATACGCCAA	AGAATTACAA	GCTAAAAATG	TCAAaGCTAT	TGTAGTcCTt
Consensus	*****-***	*****-***	*****-***	****-*****	*****-***
751					
msa237456.2{328_1169NT}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_2603}	GCaCATGTAC	CTGCAACAAG	tAAaaATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_18RS21}	GcTcATGTAC	CTGCAACAAG	cAAggATGAT	ATTGCTGAAG	GTGAAGCAGC

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_H36B}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_COH1}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M732}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_M781}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_JM9130013}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_A909}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_090}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
msa237456.2{328_CJB110}	GctCATGTAC	CTGCAACAAG	cAaggATGAT	ATTGCTGAAG	GTGAAGCAGC
Consensus	**-*****	*****	-*-*****	*****	*****
msa237456.2{328_1169NT}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_2603}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_18RS21}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_H36B}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_COH1}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M732}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_M781}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_JM9130013}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_A909}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_090}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
msa237456.2{328_CJB110}	AGAAATGATG	AAAAAAGTCA	ATCAACTCTT	CCCTGAAAAT	AGCGTAGATA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_2603}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_18RS21}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_H36B}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_COH1}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M732}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_M781}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_JM9130013}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_A909}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_090}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
msa237456.2{328_CJB110}	TTGTCCTTGC	TGGACACAAT	CATCAATATA	CAAATGGTCT	TGTTGGTAAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_2603}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_18RS21}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_H36B}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_COH1}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_M732}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_M781}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_JM9130013}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_A909}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_090}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
msa237456.2{328_CJB110}	ACTCGATTG	TACAAGCGCT	CTCTCAAGGA	AAAGCCTATG	CTGATGTACG
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_2603}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_18RS21}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_H36B}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_COH1}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M732}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_M781}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_JM9130013}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_A909}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_090}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
msa237456.2{328_CJB110}	TGGTGTCTTA	GATACTGATA	CACAAGATTT	CATTGaaACC	CCTTCAGCTA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_2603}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_18RS21}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_H36B}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_COH1}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M732}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_M781}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_JM9130013}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_A909}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_090}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
msa237456.2{328_CJB110}	AAGTAaTTGC	AGTTGCTCCT	GGTAAAAAAA	CAGGTAGTGC	CGATATTCAA
Consensus	*****	*****	*****	*****	*****
msa237456.2{328_1169NT}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_2603}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_18RS21}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_H36B}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_COH1}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M732}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_M781}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_JM9130013}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_A909}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_090}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
msa237456.2{328_CJB110}	GCCATTGTTG	ACCAAGCTAA	TACTATCGTT	AAACAAGTAA	CAGAAGCTAA
Consensus	*****	*****	*****	*****	*****
1101					
msa237456.2{328_1169NT}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_2603}	AATTGGTACT	GCCGAGGTAA	GTGtCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_18RS21}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_H36B}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_COH1}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M732}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_M781}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_JM9130013}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_A909}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_090}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
msa237456.2{328_CJB110}	AATTGGTACT	GCCGAGGTAA	GTGgCATGAT	TACGCGTTCT	GTTGATCAAG
Consensus	*****	*****	***_*****	*****	*****
1151					
msa237456.2{328_1169NT}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_2603}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_18RS21}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_H36B}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_COH1}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M732}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_M781}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_JM9130013}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_A909}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_090}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
msa237456.2{328_CJB110}	ATAATGTTAG	TCCgGTAGGC	AGCCTCATCA	CAGAGGCTCA	ACTAGCAATT
Consensus	*****	***_*****	*****	*****	*****
1201					
msa237456.2{328_1169NT}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_2603}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_18RS21}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_H36B}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_COH1}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M732}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_M781}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_JM9130013}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_A909}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_090}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
msa237456.2{328_CJB110}	GCTCGAAAAA	GCTGGCCAGA	TATCGATTTT	GCCATGACAA	ATAATGGTGG
Consensus	*****	*****	*****	*****	*****
1251					
msa237456.2{328_1169NT}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_2603}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_18RS21}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_H36B}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_COH1}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M732}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_M781}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_JM9130013}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_A909}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_090}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
msa237456.2{328_CJB110}	CATTGCTGCT	GACTTACTCA	TCAAACCAGA	TGGAACAATC	ACCTGGGGAG
Consensus	*****	*****	*****	*****	*****
1301					
msa237456.2{328_1169NT}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_2603}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_18RS21}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_H36B}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_COH1}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M732}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_M781}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_JM9130013}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_A909}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_090}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
msa237456.2{328_CJB110}	CTGCACAAGC	AGTTCAACCT	TTTGGTAATA	TCTTACAAGT	CGTCGAAATT
Consensus	*****	*****	*****	*****	*****
1351					
msa237456.2{328_1169NT}	ACTGGTAGAG	ATCTTTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAACA
1400					

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_2603}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_18RS21}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_H36B}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_COH1}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_M732}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_M781}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_JM9130013}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_A909}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_090}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
msa237456.2{328_CJB110}	ACTGGTAGAG	ATCITTATAA	AGCACTCAAC	GAACAATACG	ACCAAAAAACA
Consensus	*****	*****	*****	*****	*****
	1401			1450	
msa237456.2{328_1169NT}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_2603}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_18RS21}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_H36B}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_COH1}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M732}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_M781}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_JM9130013}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_A909}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_090}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
msa237456.2{328_CJB110}	AAATTTCTTC	CTTCAAATAG	CTGGTCTGCG	ATACACTTAC	ACAGATAATA
Consensus	*****	*****	*****	*****	*****
	1451			1500	
msa237456.2{328_1169NT}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_2603}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_18RS21}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_H36B}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_COH1}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_M732}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_M781}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_JM9130013}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_A909}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_090}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
msa237456.2{328_CJB110}	AAGAGGCGG	gGAAGAAACA	CCATTTAAAG	TTGTAAGAGC	TTATAAATCA
Consensus	*****	-*****	*****	*****	*****
	1501			1550	
msa237456.2{328_1169NT}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_2603}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_18RS21}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_H36B}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_COH1}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M732}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_M781}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_JM9130013}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_A909}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_090}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
msa237456.2{328_CJB110}	AATGGTGAGG	AAATCAATCC	TGATGCAAAA	TACAAATTAG	TTATCAATGA
Consensus	*****	*****	*****	*****	*****
	1551			1600	
msa237456.2{328_1169NT}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_2603}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_18RS21}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_H36B}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_COH1}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M732}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_M781}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_JM9130013}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_A909}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_090}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
msa237456.2{328_CJB110}	CTTTTATTTC	GGTGGTGGTG	ATGGCTTTGC	AAGCTTCAGA	AATGCCAAAC
Consensus	*****	*****	*****	*****	*****
	1601			1650	
msa237456.2{328_1169NT}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_2603}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_18RS21}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_H36B}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_COH1}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M732}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_M781}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_JM9130013}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_A909}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_090}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
msa237456.2{328_CJB110}	TTCTAGGAGC	CATTAAcCCC	GATACAGAGG	TATTTATGGC	CTATATCACT
Consensus	*****	*****	*****	*****	*****
	1651			1700	

Table 71: Comparative Sequences relating to SAG1333

msa237456.2{328_1169NT}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_2603}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_18RS21}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_H36B}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_COH1}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M732}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_M781}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	aTTCCAAATA	ATAAACCTAA
msa237456.2{328_JM9130013}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_A909}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_090}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
msa237456.2{328_CJB110}	GATTTAGAAA	AAGCTGGTAA	AAAAGTGAGC	gTTCCAAATA	ATAAACCTAA
Consensus	*****	*****	*****	-*****	*****
1701		1750			
msa237456.2{328_1169NT}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_2603}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_18RS21}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_H36B}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_COH1}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_M732}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_M781}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_JM9130013}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_A909}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_090}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
msa237456.2{328_CJB110}	AATCTATGTC	ACTATGAAGA	TGGTTAATGA	AACTATTACA	CAAAATGATG
Consensus	*****	*****	*****	*****	*****
1751		1800			
msa237456.2{328_1169NT}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_2603}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_18RS21}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_H36B}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_COH1}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M732}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_M781}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_JM9130013}	GTACACATAG	CATTATTgAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_A909}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_090}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
msa237456.2{328_CJB110}	GTACACATAG	CATTATTaAG	AAACTTTTATT	TAGATCGACA	AGGAAATATT
Consensus	*****	*****	*****	*****	*****
1801		1850			
msa237456.2{328_1169NT}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_2603}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_18RS21}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_H36B}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_COH1}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M732}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_M781}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_JM9130013}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_A909}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_090}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
msa237456.2{328_CJB110}	GTAGCACAAG	AGATTGTATC	AGACACTTTA	AACCAAACAA	AATCAAATC
Consensus	*****	*****	*****	*****	*****
1851		1900			
msa237456.2{328_1169NT}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_2603}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_18RS21}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_H36B}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_COH1}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M732}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_M781}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_JM9130013}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_A909}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_090}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
msa237456.2{328_CJB110}	TACAAAAATC	AACCCTGTAA	CTACAATTCA	CAAAAAACAA	TTACACCAAT
Consensus	*****	*****	*****	*****	*****
1901		1950			
msa237456.2{328_1169NT}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_2603}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_18RS21}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_H36B}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_COH1}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M732}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_M781}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_JM9130013}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_A909}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_090}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
msa237456.2{328_CJB110}	TTACAGCTAT	TAACCCTATG	AGAAATTATG	GCAAACCATC	AAACTCCACT
Consensus	*****	*****	*****	*****	*****

Table 71: Comparative Sequences relating to SAG1333

	1951			2000
msa237456.2{328_1169NT}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_2603}	ACTGTAAAT CAaaACAAtt	accaaaaaaca	aactctgaat	atggacaatc
msa237456.2{328_18RS21}	ACTGTAAAT CAaaa-----	-----	-----	-----
msa237456.2{328_H36B}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_COH1}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_M732}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_M781}	ACTGTAAAT CAaa-----	-----	-----	-----
msa237456.2{328_JM9130013}	ACTGTAAAT CAaaa-----	-----	-----	-----
msa237456.2{328_A909}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_090}	ACTGTAAAT CAaaACAA--	-----	-----	-----
msa237456.2{328_CJB110}	ACTGTAAAT CA-----	-----	-----	-----
Consensus	***** **_*****	*****	*****	*****
	2001			2050
msa237456.2{328_1169NT}	attccttatg	tctgtctttg	gtggttgact	tataggaatt
msa237456.2{328_2603}	-----	-----	-----	gctttaaata
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	*****	*****
	2051			2070
msa237456.2{328_1169NT}	-----	-----	-----	-----
msa237456.2{328_2603}	caaagaaaa	acatatgaaa	-----	-----
msa237456.2{328_18RS21}	-----	-----	-----	-----
msa237456.2{328_H36B}	-----	-----	-----	-----
msa237456.2{328_COH1}	-----	-----	-----	-----
msa237456.2{328_M732}	-----	-----	-----	-----
msa237456.2{328_M781}	-----	-----	-----	-----
msa237456.2{328_JM9130013}	-----	-----	-----	-----
msa237456.2{328_A909}	-----	-----	-----	-----
msa237456.2{328_090}	-----	-----	-----	-----
msa237456.2{328_CJB110}	-----	-----	-----	-----
Consensus	*****	*****	-----	-----

SEQ ID NO. 7112

STRAIN 2603 frame: 1

MKKKI ILKSSVGLVAGTSMFSSVFADQVGVQVIGVNDPHGALDNTGTANMPDGKVVANA
GTAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMVGPANSGLLQDEPTVKNFNAMNVE
YGTLDGHEFDEGLAEYNRIVTGKAPAPDSNINNTKSPHEAAKQEI VVANVIDKVNKQI
PYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLVLRKNYEQYEFLEAETIVKYAKELQ
AKNVKAVVLAHVPAATSKNDIAEGEAAEMMKVNLFPENSVDIVFAGHNHQYTNGLVKG
TRIVQALSQKAYADVRGVLDTDTQDFIETPSAKVIAVAPGKKTGSADIQAI VQDQANTIV
KQVTEAKIGTAEVSGMITSVDQDNVSPVGSGLITAEQLAIARKSWPIDFAMTNNGGIRAD
LLIKPDGTITWGAAQAVQVPGNIIQVVEITGRDLYKALNEQYDQKQNFLLQIAGLRYTY
TDNKEGGEETPFKVVKAYKSNGBEINPDAKYKLVINDFLFGGGDGFASFRNAKLLGAINP
DTEVFMAIITDLEKAGKKSVPNNKPKIYVTMKNVNETITQNDGTHSIIKLYLDRQGNIV
AQEIVSDTLNQTQKSKSTKINPVTTIHKKQLHQFTAIPMRNYGKPSNSTTVKSKQLPKT
NSEYQSFLMSVFGVGLIGIALNTKKKHKM

SEQ ID NO. 7113

STRAIN 090 frame: 3

VGVQVIGVNDPHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRV
QAGDMVGPANSGLLQDEPTVKTNFAMNVEYGTLDGHEFDEGLAEYNRIVTGKAPAPDS
NINNTKSPHEAAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNNKSVNVGFIGIVTK
DIPNLVLRKNYEQYEFLEAETIVKYAKELQAKNVKAVVLAHVPAATSKDDIAEGEAAEM
MKVNLFPENSVDIVFAGHNHQYTNGLVKGTRIVQALSQKAYADVRGVLDTDTQDFIET
TPSAKVVAVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITSVDQDNVSPV
GSLITAEQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQVPGNIIQVVE
ITGRDLYKALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPD
KYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAIITDLEKAGKKSVPNNKPKIY
VTMKNVNETITQNDGTHSIIKLYLDRQGNIVAQEIVSDTLNQTQKSKSTKINPVTTIHKK
QLHQFTAIPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7114

STRAIN A909 frame: 3

VNDFHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQAGDMV
ASPANSGLLQDEPTVKTNFAMNVEYGTLDGHEFDEGLAEYNRIVTGKAPAPDSNINNTK
SPHEAAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNNKSVNVGFIGIVTKDIPNLV
RKNYEQYEFLEAETIVKYAKELQAKNVKAVVLAHVPAATSKDDIAEGEAAEMMKVNL
FPENSVDIVFAGHNHQYTNGLVKGTRIVQALSQKAYADVRGVLDTDTQDFIETPSAKVI
AVAPGKKTGSADIQAI VQDQANTIVKQVTEAKIGTAEVSGMITSVDQDNVSPVGSGLIT
AEQLAIARKSWPIDFAMTNNGGIRADLLIKPDGTITWGAAQAVQVPGNIIQVVEITGRDLY
KALNEQYDQKQNFLLQIAGLRYTYTDNKEGGEETPFKVVKAYKSNGBEINPDAKYKLVIN
DTEVFMAIITDLEKAGKKSVPNNKPKIYVTMKNVNETITQNDGTHSIIKLYLDRQGNIV
AQEIVSDTLNQTQKSKSTKINPVTTIHKKQLHQFTAIPMRNYGKPSNSTTVKSKQ

Table 71: Comparative Sequences relating to SAG1333

INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7115

STRAIN H36B frame: 2

QVGVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNIITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYT I KNI PVNNKSVNVGFIGIVT
KDI PNLVLRKKNYQYEFLEDEAET I VKYAKELQAKNVKAI VVLAHV PATSKDDI AEGEAAE
MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQ GKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI VDOQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSP
VGS LI TEAQLAI ARKSWPDI DFAMTNNGG I RADLLI KPDGTITWGAAQAVQPPFGN ILQVV
EITGRDLYKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTVEVF MAYITDLEKAGK KVSVPNNKPKI
YVTMKNVNETITQNDGTYSI I KKL YLDRQGN I VAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKS

SEQ ID NO. 7116

STRAIN 18RS21 frame: 1

DOVGVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGLGNHEFDEGLAEYNRIVTGKAPAP
DSNINNIITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYT I KNI PVNNKSVNVGFIGIV
TKDI PNLVLRKKNYQYEFLEDEAET I VKYAKELQAKNVKAI VVLAHV PATSKDDI AEGEAA
EMMKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQ GKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI VDOQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSP
VGS LI TEAQLAI ARKSWPDI DFAMTNNGG I RADLLI KPDGTITWGAAQAVQPPFGN ILQVV
VEITGRDLYKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTVEVF MAYITDLEKAGK KVSVPNNKPKI
IYVTMKNVNETITQNDGTYSI I KKL YLDRQGN I VAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKSK

SEQ ID NO. 7117

STRAIN M732 frame: 3

QVGVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNIITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYT I KNI PVNNKSVNVGFIGIVT
KDI PNLVLRKKNYQYEFLEDEAET I VKYAKELQAKNVKAI VVLAHV PATSKDDI AEGEAAE
MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQ GKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI VDOQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSP
VGS LI TEAQLAI ARKSWPDI DFAMTNNGG I RADLLI KPDGTITWGAAQAVQPPFGN ILQVV
EITGRDLYKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTVEVF MAYITDLEKAGK KVSVPNNKPKI
YVTMKNVNETITQNDGTYSI I KKL YLDRQGN I VAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKSKQ

SEQ ID NO. 7118

STRAIN COH1 frame: 3

QVGVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNIITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYT I KNI PVNNKSVNVGFIGIVT
KDI PNLVLRKKNYQYEFLEDEAET I VKYAKELQAKNVKAI VVLAHV PATSKDDI AEGEAAE
MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQ GKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI VDOQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSP
VGS LI TEAQLAI ARKSWPDI DFAMTNNGG I RADLLI KPDGTITWGAAQAVQPPFGN ILQVV
EITGRDLYKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTVEVF MAYITDLEKAGK KVSVPNNKPKI
YVTMKNVNETITQNDGTYSI I KKL YLDRQGN I VAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKS

SEQ ID NO. 7119

STRAIN M781 frame: 1

QVGVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGLGNHEFDEGLAEYNRIVTGKAPAPD
SNINNIITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYT I KNI PVNNKSVNVGFIGIVT
KDI PNLVLRKKNYQYEFLEDEAET I VKYAKELQAKNVKAI VVLAHV PATSKDDI AEGEAAE
MMKKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQ GKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI VDOQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSP
VGS LI TEAQLAI ARKSWPDI DFAMTNNGG I RADLLI KPDGTITWGAAQAVQPPFGN ILQVV
EITGRDLYKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTVEVF MAYITDLEKAGK KVSVPNNKPKI
YVTMKNVNETITQNDGTYSI I KKL YLDRQGN I VAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKS

SEQ ID NO. 7120

STRAIN CJB110 frame: 1

DOVGVQVIGVNDPFGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESI
RVQAGDMVGASPANSGLLQDEPTVKTFNAMNVEYGLGNHEFDEGLAEYNRIVTGKAPAP
DSNINNIITKSYPHAAKQEI VVANVIDKVNKQI PYNWKPYT I KNI PVNNKSVNVGFIGIV
TKDI PNLVLRKKNYQYEFLEDEAET I VKYAKELQAKNVKAI VVLAHV PATSKDDI AEGEAA
EMMKVNQLFPENSVDI VFAGHNHQYTNGLVGKTRI VQALSQ GKAYADVRGVLDTDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI VDOQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSP
VGS LI TEAQLAI ARKSWPDI DFAMTNNGG I RADLLI KPDGTITWGAAQAVQPPFGN ILQVV
VEITGRDLYKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTVEVF MAYITDLEKAGK KVSVPNNKPKI
YVTMKNVNETITQNDGTYSI I KKL YLDRQGN I VAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKS

Table 71: Comparative Sequences relating to SAG1333

DAKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKVKVSPNNKPKI
YVTMKNVNETITQNDGTHSI I KKL YLDRQGNIVAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKS

SEQ ID NO. 7121

STRAIN 1169NT frame: 1

QVGVQVIGVNDPHGALDNTGTANMPDGKVKVANAGTAAQLDAYMDDAQKDFKQTNPNGESIR
VQAGDMVGASPANSGLLQDEPTVKnFNAMNVEYGTlGNHEFDEGLAEYNRIVTGKAPAPD
SNINNITKSYPHAEAAKQEI VVANVIDKVNKQI PYNWKPYAIKNI PVNKNKSVNVGFIGIVT
KDI PNLVLRKNYEQYEFLEAETI VKYAKELQAKNVKAI VVLAHV PATSKNDIAEGEAAE
MMKKVNQLFPENSVDIVFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDDTQDFI
ETPSAKVIAVAPGKKTGSADI QAI V DQANT I VKQVTEAKI GTAEVSVMI TRSVDQDNVSP
VGS LITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAQAQVQPFNGNILQVV
EITGRDL YKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPD
AKYKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKVKVSPNNKPKI
YVTMKNVNETITQNDGTHSI I KKL YLDRQGNIVAQEI VSDTLNQT KSKSTKINPVTTIHK
KQLHQFTA INPMRNYGKPSNSTTVKS

SEQ ID NO. 7122

STRAIN JM9130013 frame: 2

GVQVIGVNDPHGALDNTGTANMPDGKVTNAGTAAQLDAYMDDAQKDFKQTNPNGESIRVQ
AGDMVGASPANSGLLQDEPTVKTFNAMNVEYGTlGNHEFDEGLAEYNRIVTGKAPAPDSN
INNITKSYPHAEAAKQEI VVANVIDKVNKQI PYNWKPYTIKNI PVNKNKSVNVGFIGIVTKD
IPNLVLRKNYEQYEFLEAETI VKYAKELQAKNVKAI VVLAHV PATSKDDIAEGEAAEMM
KKNVQLFPENSVDIVFAGHNHQYTNGLVGKTRI VQALSQGKAYADVRGVLDDTQDFIET
PSAKVIAVAPGKKTGSADI QAI V DQANT I VKQVTEAKI GTAEVSGMI TRSVDQDNVSPV
SLITEAQLAIARKSWPDI DFAMTNNGGIRADLLIKPDGTITWGAQAQVQPFNGNILQVVIE
TGRDL YKALNEQYDQKQNFLLQIAGLR YTYTDNKEGGEETPFKVVKAYKSNGBEINPDAK
YKLVINDFLFGGGDGFASFRNAKLLGAINPDTEVFMAYITDLEKAGKVKVSPNNKPKI YV
TMKNVNETITQNDGTHSI I EKL YLDRQGNIVAQEI VSDTLNQT KSKSTKINPVTTIHKKQ
LHQFTA INPMRNYGKPSNSTTVKSK

PRETTY of: /biotmp/msa237615.2{*} May 14, 2003 03:22 ..

msa237615.2{328_1169NT} i 50
msa237615.2{328_2603} -----qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_A909} mkkkiilkss vglvagtai mfsvfaDqv gvqvigVNDF HGALDNTGTA
msa237615.2{328_M732} -----VNDF HGALDNTGTA
msa237615.2{328_M732} -----qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_COH1} -----qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_M781} -----qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_H36B} -----qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_JM9130013} -----qv gvqvigVNDF HGALDNTGTA
msa237615.2{328_18RS21} -----Dqv gvqvigVNDF HGALDNTGTA
msa237615.2{328_090} -----v gvqvigVNDF HGALDNTGTA
msa237615.2{328_CJB110} -----Dqv gvqvigVNDF HGALDNTGTA
Consensus *****-*****-*****-*****-*****

msa237615.2{328_1169NT} 51 100
msa237615.2{328_2603} NMPDGKVaNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_A909} NMPDGKVaNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_M732} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_COH1} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_M781} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_H36B} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_JM9130013} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_18RS21} NMPDGKvXNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_090} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
msa237615.2{328_CJB110} NMPDGKvTNA GTAAQLDAYM DDAQKDFKQT NPNGESIRVQ AGDMVGASPA
Consensus *****-*****-*****-*****-*****

msa237615.2{328_1169NT} 101 150
msa237615.2{328_2603} NSGLLQDEPT VKnFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_A909} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_M732} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_COH1} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_M781} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_H36B} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_JM9130013} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_18RS21} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_090} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
msa237615.2{328_CJB110} NSGLLQDEPT VktFNAMNVE YGTlGNHEFD EGLAEYNRIV TGKAPAPDSN
Consensus *****-*****-*****-*****-*****

msa237615.2{328_1169NT} 151 200
msa237615.2{328_2603} INNITKSYPH EAAKQEI VVA NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
msa237615.2{328_A909} INNITKSYPH EAAKQEI VVA NVIDKVNKQI PYNWKPYaIK NIPVNNKSVN
msa237615.2{328_M732} INNITKSYPH EAAKQEI VVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
msa237615.2{328_COH1} INNITKSYPH EAAKQEI VVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN
msa237615.2{328_M781} INNITKSYPH EAAKQEI VVA NVIDKVNKQI PYNWKPYtIK NIPVNNKSVN

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_H36B}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_JM9130013}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_18RS21}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYtIK	NIPVNNKSVN
msa237615.2{328_090}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
msa237615.2{328_CJB110}	INNITKSYPH	EAAKQEI VVA	NVIDKVNKQI	PYNWKPYaIK	NIPVNNKSVN
Consensus	*****	*****	*****	*****_*	*****
201					
msa237615.2{328_1169NT}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_2603}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_A909}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M732}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_COH1}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_M781}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_H36B}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_JM9130013}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_18RS21}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_090}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
msa237615.2{328_CJB110}	VGFIGIVTKD	IPNLVLRKNY	EQYEFLEDEAE	TIVKYAKELQ	AKNVKAI VVL
Consensus	*****	*****	*****	*****	*****
251					
msa237615.2{328_1169NT}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_2603}	AHVPATSKnD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_A909}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_M732}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_COH1}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_M781}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_H36B}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_JM9130013}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_18RS21}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_090}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
msa237615.2{328_CJB110}	AHVPATSKGD	IAEGEAAEMM	KKVNQLFPEN	SVDIVFAGHN	HQYTNGLV GK
Consensus	*****	*****	*****	*****	*****
301					
msa237615.2{328_1169NT}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_2603}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_A909}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_M732}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_COH1}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_M781}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_H36B}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_JM9130013}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_18RS21}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_090}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
msa237615.2{328_CJB110}	TRIVQALSQ	KAYADVRGVL	DTDTQDFIET	PSAKVI AVAP	GKKTGSADI Q
Consensus	*****	*****	*****	*****_****	*****
351					
msa237615.2{328_1169NT}	AIVDQANTIV	KQVTEAKIGT	AEVSVMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_2603}	AIVDQANTIV	KQVTEAKIGT	AEVSVMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_A909}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M732}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_COH1}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_M781}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_H36B}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_JM9130013}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_18RS21}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_090}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
msa237615.2{328_CJB110}	AIVDQANTIV	KQVTEAKIGT	AEVSGMITRS	VDQDNVSPVG	SLITEAQLAI
Consensus	*****	*****	*****_****	*****	*****
401					
msa237615.2{328_1169NT}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_2603}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_A909}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M732}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_COH1}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_M781}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_H36B}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_JM9130013}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_18RS21}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_090}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
msa237615.2{328_CJB110}	ARKSWPDIDF	AMTNNGGIRA	DLLIKPDGTI	TWGAAQAVQP	FGNILQVVEI
Consensus	*****	*****	*****	*****	*****
451					
msa237615.2{328_1169NT}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_2603}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_A909}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_M732}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS
msa237615.2{328_COH1}	TGRDLYKALN	EQYDQKQNF	LQIAGLRITY	TDNKEGG EET	PFKVVKAYKS

Table 71: Comparative Sequences relating to SAG1333

msa237615.2{328_M781}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_H36B}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_JM9130013}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_18RS21}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_090}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
msa237615.2{328_CJB110}	TGRDLYKALN	EQYDQKQNF	LQIAGLRYTY	TDNKEGGEET	PFKVVKAYKS
Consensus	*****	*****	*****	*****	*****
	501				550
msa237615.2{328_1169NT}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_2603}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_A909}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M732}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_COH1}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_M781}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_H36B}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_JM9130013}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_18RS21}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_090}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
msa237615.2{328_CJB110}	NGEEINPDAK	YKLVINDFLF	GGGDGFASFR	NAKLLGAINP	DTEVFMAYIT
Consensus	*****	*****	*****	*****	*****
	551				600
msa237615.2{328_1169NT}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_2603}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_A909}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_M732}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_COH1}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_M781}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_H36B}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_JM9130013}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_18RS21}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_090}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
msa237615.2{328_CJB110}	DLEKAGKKVS	VPNNKPKIYV	TMKMVNETIT	QNDGThSIIk	KLYLDRQGNI
Consensus	*****	*****	*****	*****	*****
	601				650
msa237615.2{328_1169NT}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_2603}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_A909}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M732}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_COH1}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_M781}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_H36B}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_JM9130013}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_18RS21}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_090}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
msa237615.2{328_CJB110}	VAQEIVSDTL	NQTKSKSTKI	NPVTTIHKKQ	LHQFTAINPM	RNYGKPSNST
Consensus	*****	*****	*****	*****	*****
	651				690
msa237615.2{328_1169NT}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_2603}	TVKSKQlpkt	nseygqsflm	svfvgvligi	alntkckhmk	-----
msa237615.2{328_A909}	TVKSKQ----	-----	-----	-----	-----
msa237615.2{328_M732}	TVKSKQ----	-----	-----	-----	-----
msa237615.2{328_COH1}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_M781}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_H36B}	TVKS-----	-----	-----	-----	-----
msa237615.2{328_JM9130013}	TVKSK-----	-----	-----	-----	-----
msa237615.2{328_18RS21}	TVKSK-----	-----	-----	-----	-----
msa237615.2{328_090}	TVKSKQ----	-----	-----	-----	-----
msa237615.2{328_CJB110}	TVKS-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7201

STRAIN 2603

ATGAATAAACCGGTA AAAATCGTTGCAACACTTGGTCCGCGGTTGAATCCCGTGGTG
GTAAGAAGTTTGGTGAAGTCTGGATACTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAG
AAAAATTGCTCAATTGATTAAGAAGGTTGCTAACGTTTTCCGTTTCAACTTCTCACATG
GAGATCATGCTGAGCAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAGAGATGCGAG
GACAAAAAGTTGGCTTCCCTCTTGATACTAAAGGACCTGAATTCGTACAGAACTTTTTG
AAGATGGTGCAGATTTCCATTTCATATACAACAGGTACAAAAATACGTGTTGCTACTAAGC
AAGGTATCAAATCACTCCAGAAGTGATTGCAITGAAITGTTGCTGGTGGACTTGACATCT
TTGATGACGTTGAAGTTGGTAAGCAAATCCTTGTGTGATGATGGTAAACTAGGCTTACTG
TGTTTGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCCCTTA
TTGGTAAACAAAAGGTTGTAACATCCCTTATACTAAATTCCTTTCCAGCACTTGCGAG
AACGCGATAATGCTGATACCGTTTTGGACTTGAGCAAGGACTTAACTTTATTGCTATCT
CATTTGTACGTACTGCTAAAAGATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGsm
ATGGACACGTTAAGTTGTTTCTAAAATGAAATCAACAAGGTATCGATAATATGATG
AGATTTATCGAAGCAGCAGATGGTATTTATGATTGCTCGTGGTGATATGGGTATCGAAGTTC
CATTTGAAATGTTTCCAGTTTACCAAAAATGATCATTACTAAAGTTAATGCAGCTGGTFA
AAGCAGTTATTACAGCAACAAATATGCTTgAAAACAATGACTGATAAACCCGTCGCGACTC
GTTCAGAAGTATCTGATGCTTCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTT
CAGGTGAGTCAGCTAATGGTAAATACCCAGTTGAGTCAGTTGTAACAATGGCTACTATG
ATAAAAATGCTCAACATTACTCAATGAGTATGGTTCGCTAGACTCAATGCTGCAATCCAC
GTAATAACAAAATGATGTTATTGCACTGCGGTTAAAGATGCAACACACTCAATGGATA
TCAAACCTTGTGTAAACAATTAAGTAAACAGGTAATACAGCTCGTGCCATTTCTAAATCC
GTCCAGATGCACACATTTTGGCTGTTACATTTGATGAAAAAGTACAAACGTTCAATGATGA
TTAACTGGGGTGTATCCCTGCTTTCAGACAAAACAGCATCTACAGATGATATGTTTG
AGGTTGCAGAAGCTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTTA
TCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACATAACAATGCGTGTTCGTACTGTTA
AA

SEQ ID NO. 7202

STRAIN 090

AATAAACCGGTA AAAATCGTTGCAACACT
TGGTCCGCGGTAGAATTCGGTGGTGGTAAGAAGTTTGGTGAAGTCTGGAT
ACTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCTCAA
TTGATTAAGAAGGTTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGA
TCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAGAGA
TTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACTGAAAT
CGTACAGAACTTTTTGAAGATGGTTGAGATTTCCATTTCATATACAACAGG
TACAGAATTACGTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAG
TGATTTGCATTTGAATGTTGCTGGTGGACTTGACATCTTTGATGAGCTTGAA
GTTGGTAAAGCAATCCTTGTGATGATGGTAAACTAGGCTTACTGTGTT
TGCAAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATG
GCCTTATTGGTAAACAaaaaGGTGTAAACATCCCTTATACTAaaAATTCCT
TTCCCAgCACTTGCAAGCAGGATAATGCTGATATCCGTTTTGGACTTGA
GCAAGGACTTAACTTTATTGCTATCTCATTGTACGTACTGCTAAAGATG
TTAATGAAGTTCGTGCTATTGTTGAAGAAACTGGCAATGGACATGTTAAG
TTGTTTGTCTAAAATGAAAAATCAACAAGGTATCGATAATATTGATGAGAT
TATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTGAATGAGGTTATCG
AAGTTCCATTGAAAATGGTTCCAGTTTACCAAAAATGATCATTACTAAA
GTTAATGAGCTGGTAAAGCAGTTATTACAGCAACAATATGCTTGAAC
AATGACTGATAAACCCGTCGACTCGTTGAGAAATCTGATGTTCTTCA
ATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCAGCT
AATGGTAAATACCCAGTTGAGTCAGTTGCTACAATGGCTACTATTGATAA
AAATGCTCAAACATTAATCAATGATGATGGTTCGCTTAGACTCATCTGCAT
TCCACGTAATAACAAAATGATGTTATTGCACTGCGGTTAAAGATGCA
ACACACTCAATGGATATCAAACCTTGTGTGACAATTAAGTAAACAGGTA
TACAGCTCGTGCCATTTCTAAATTCGCTCCAGATGCAGACATTTTGGCTG
TTACATTTGATGAAAAAGTACAACGTTCAATGATGATTAACCTGGGGTGT
ATCCCTGTCCTTGACAGCAAAACAGCATCTACAGATGATATGTTGAGGT
TGCAAGCAGTGTAGCACTTGAAGCAGGACTTGTGAAATCAGGCGATAATA
TCGTTATCGTTGAGGTGTTCTGTAGGTACAGGTGGAACATAACAATG
CGTCTTCTACTGTTAAA

SEQ ID NO. 7203

STRAIN A909

AATAAACCGGTA AAAATCGTTGCAACACTTGGTC
CTGCGGTTGAATTCGGTGGTGAAGAAGTTTGGTGAAGTCTGGTACTG
GGTGAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCTCAATTGAT
TAAAGAAGGTTGCTAACGTTTTCCGTTTCAACTTCTCACATGGAGATCATG
CTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAGAGATGCA
GGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAAATTCGTAC
AGAACTTTTTGAAGATGGTGCAGATTTCCATTTCATATACAACAGGTACAA
AATTACGTTGTTGCTACTAAGCAAGGTATCAAATCACTCCAGAAGTGATT
GCAITGAAATGTTGCTGGTGGACTTGACATCTTTGATGACGTTGAAGTTGG
TAAGCAAACTCCTTGTGATGATGGTAAACTAGGTTCTACTGTTTTCGAA
AAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATGATGGCTTT
ATTGGTAAACAAAAAGGTTGTAACATCCCTTATACTAAAAATTCCTTTCC
AGCACTTGCAAGACGCGATAATGCTGATATCCGTTTTGGACTTGAGCAAG
GACTTAACTTTATTGCTATCTCATTGTACGTAAGTACTGCTAAAGATGTTAAT
GAAGTTCCGTGCTATTGTTGAAGAACTGGCAATGGACAGGTTAAGTTGTT
TGCTAAAATGAAAATCAACAAGGTATCGATAATATTGATGAGATTATCG
AAGCAGCAGATGGTATTATGATTGCTCGTGGTGAATGGGTATCGAAGTT
CCATTGAAATGTTCCAGTTTACCAAAAATGATCATTACTAAAAGTTAA

Table 72: Comparative Sequences relating to SAG0941

TGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGAACAATGA
CTGATAAACCCGCTGCGACTCGTTTCAGAAAGTATCTGATGTCTTCAATGCT
GTTATTGATGGTACTGATGCTACAATGCTTTTCAGGTGAGTCAGCTAATGG
TAATACCAGTTGAGTCAGTTCCGTACAATGGCTACTATTGATAAAAAATG
CTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTGCATTCCCA
CGTAATAACAAAACCTGATGTTATTGCACTGCGGTTAAAGATGCAACACA
CTCAATGGATATCAAACCTGTTGTAACAATTAAGTAAACAGGTAATACAG
CTCGTGCCATTTCTAAATCCGTCAGATGCAGACATTTTGGCTGTTACA
TTTGATGAAAAAGTACAACGTTTCATTGATGATTAACCTGGGGTGTATCCC
TGTCCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGGAGTTGCAG
AACGTGTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATAATATCGTT
ATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACCAATGCGTGT
TCGTACTGTTAAA

SEQ ID NO. 7204

STRAIN H36B

AATAAACCGGTAAAAATCGTTGCAAC
ACTTGGTCTGCGGTTGAATTCCTGGTGGTAAAGTTTGGTGAGTCTG
GATCTGGGGTGAAGCCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAG
AGATTGCAAGGACAAAAAGTTGGCTTCTCCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCCTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGCAAGACCGGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTGTACGTAAGCTAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
AAGTTGTTGCTAAAATGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATGATGATGCTCGTGGTGATATGGGTA
TCGAAGTTCATTGAAATGTTCCAGTTTACCAAAAAATGATCAITACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAAATGACTGATAAACCAACGTCGACTCGTTGAGAAGTATCTGATGCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CAITCCCAGTAAATAACAAAACCTGATGTTATTGCTATGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACCTGTTGTAACAATTAAGTAAACAGG
TAATACAGCTCGTGCCATTTCTAAATCCGTCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTCATTGATGATTAACCTGGGT
GTTATCCCTGCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7205

STRAIN 18RS21

AATAAACCGGTAAAAATCGTTGCAAC
ACTTGGTCTGCGGTTGAATTCCTGGTGGTAAAGTTTGGTGAGTCTG
GATACTGGGGTGAAGCCCTTGACGTAGAAGCTTCAGCAGAAAAAATTGCT
CAATTGATTAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAG
AGATTGCAAGGACAAAAAGTTGGCTTCTCCTTGATACTAAAGGACCTGAA
ATTTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTATATACAAC
AGGTACAAAAATTACGTGTTGCTACTAAGCAAGGTATCAAATCACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCCTACTGT
GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTGCAAGACCGGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACTTTATTGCTATCTCATTGTACGTAAGCTAAG
ATGTTAATGAAGTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
AAGTTGTTGCTAAAATGAAAATCAACAAGGTATCGATAATATTGATGA
GATTATCGAAGCAGCAGATGGTATGATGATGCTCGTGGTGATATGGGTA
TCGAAGTTCATTGAAATGTTCCAGTTTACCAAAAAATGATCAITACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
AACAAATGACTGATAAACCAACGTCGACTCGTTGAGAAGTATCTGATGCT
TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCAGTTCGTACAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTCGCTTAGACTCATCTG
CAITCCCAGTAAATAACAAAACCTGATGTTATTGCTATGCGGTTAAAGAT
GCAACACACTCAATGGATATCAAACCTGTTGTAACAATTAAGTAAACAGG
TAATACAGCTCGTGCCATTTCTAAATCCGTCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTCATTGATGATTAACCTGGGT
GTTATCCCTGCTTGCAGACAAACCAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTTAGCACTTGAAGCAGGATTTGTTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCTGTAGGTACAGGTGGAACCTAACACA
ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7206

Table 72: Comparative Sequences relating to SAG0941

STRAIN M732
 AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGAGATTTCCATTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCAGCACTTGAGCAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTGTGACTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGTTCCAGTTTACCACAAAATGATCACTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAAATATGCTTGA
 AACAAATGACTGATAAACCAACGTCGACTCGTTGAGAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCACTGTTTGTACAAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAATGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAAATCCGTCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAGTACAACGTTCAATTGATGATTAACCTGGGGT
 GTTATCCCTGTCCTTGCAGACAAACAGCATCTACAGATGATATGTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGACGGTGTTCCTGTAGGTACAGGTGAACTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7207

STRAIN COH1

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGAGATTTCCATTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGTAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCAGCACTTGAGCAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTGTGACTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATTGCTCGTGGTATATGGGTA
 TCGAAGTTCCATTGAAATGTTCCAGTTTACCACAAAATGATCACTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAAATATGCTTGA
 AACAAATGACTGATAAACCAACGTCGACTCGTTGAGAGTATCTGATGCT
 TCAATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCACTGTTTGTACAAATGGCTACTATTGA
 TAAAAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTAGACTCATCTG
 CATTCCCACGTAATAACAAAATGATGTTATTGCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAATGTTGTAACAATTACTGAAACAGG
 TAATACAGCTCGTGCCATTTCTAAAATCCGTCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAGTACAACGTTCAATTGATGATTAACCTGGGGT
 GTTATCCCTGTCCTTGCAGACAAACAGCATCTACAGATGATATGTTGA
 GGTTCAGAACGTTGACACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGACGGTGTTCCTGTAGGTACAGGTGAACTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7208

STRAIN M781

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCCTGCGGTAGAATTCGGTGGTGAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAGAAGGTGCTAACGTTTTCCGTTTCAACTTCTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGAGATTTCCATTATATACAAC
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTTGTTGAGAATG
 ATGGCCTTATTGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCAGCACTTGAGCAAGCGGATAATGCTGATATCCGTTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTGTGACTACTGCTAAAG

Table 72: Comparative Sequences relating to SAG0941

ATGTTAATGAAGTTCGTGCTATTTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGGCTAAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCCGAAGCAGCAGATGGTATTATGATGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTCCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGACTCGTTTCCAGAAATATCTGATGCT
 TCAATGCTGTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCAGTAATAACAAAATGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCATTTCTAAAGTCCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAAGTGGGT
 GTTATCCCTGTCCTTGAGCAAAACCCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTTATCGTTGCAAGGTGTTCCCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7209

STRAIN CJB110

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTTGAAATCCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTCAACTTTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCTTGTACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTTCATATAACA
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCAATGAAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTGTGTTGAGAATG
 ATGGCCTTATGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCCAGCACTTGCAGAACCGGATAATGCTGATATCCGTTTGGACT
 TGAAACAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTCCAGTTTACCAAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGACTCGTTTCCAGAAATATCTGATGCT
 TCAATGCTGTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCAGTAATAACAAAATGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCATTTCTAAATCCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAAGTGGGT
 GTTATCCCTGTCCTTGAGCAAAACCCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTATATCGTTGCAAGGTGTTCCCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAAA

SEQ ID NO. 7210

STRAIN I169NT

AATAAACCGGTAAAAATCGTTGCAAC
 ACTTGGTCTCGCGTAGAATCCCGTGGTGGTAAGAAGTTTGGTGAGTCTG
 GATACTGGGGTGAAAGCCTTGACGTAAGAAGCTTCAGCAGAAAAAATGCT
 CAATTGATTAAAGAAGGTGCTAACGTTTCCGTTCAACTTTCACATGG
 AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAG
 AGATTGCAGGACAAAAAGTTGGCTTCTCTTGTACTAAAGGACCTGAA
 ATTCGTACAGAACTTTTGAAGATGGTGCAGATTTCCATTTCATATAACA
 AGGTACAAAATTACGTTGCTACTAAGCAAGGTATCAAATCAACTCCAG
 AAGTGATTGCAATGAAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
 GAAGTTGGTAAGCAAATCCTTGTGATGATGGTAACTAGGTCTTACTGT
 GTTTGCAAAAGATAAAGACACTCGTGAATTTGAAGTAGTGTGTTGAGAATG
 ATGGCCTTATTTGGTAAACAAAAGGTGTAACATCCCTTATACTAAAATT
 CCTTCCCAGCACTTGCAGAACCGGATAATGCTGATATCCGTTTGGACT
 TGAGCAAGGACTTAACTTTATTGCTATCTCATTTGTACGTACTGCTAAAG
 ATGTTAATGAAGTTTCGTGCTATTTGTGAAGAACTGGCAATGGACACGTT
 AAGTTGTTTGGCTAAAATTGAAAATCAACAAGGTATCGATAATATTGATGA
 GATTATCGAAGCAGCAGATGGTATTATGATGCTCGTGGTGATATGGGTA
 TCGAAGTTCATTGAAATGGTCCAGTTTACCAAAAATGATCATTACT
 AAAGTTAATGCAGCTGGTAAAGCAGTTATTACAGCAACAAATATGCTTGA
 AACAAATGACTGATAAACCCAGTGGACTCGTTTCCAGAAATATCTGATGCT
 TCAATGCTGTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
 GCTAATGGTAAATACCCAGTTGAGTCAGTTTCGTACAATGGCTACTATTGA
 TAAAAATGCTCAAACTTACTCAATGAGTATGGTCGCTTAGACTCATCTG
 CATTCCCAGTAATAACAAAATGATGTTATTGTCATCTGCGGTTAAAGAT
 GCAACACACTCAATGGATATCAAACTTGTGTAAACAATTACTGAAACAGG
 TAATACAGCTCGTGCATTTCTAAATCCCGTCCAGATGCAGACATTTTGG
 CTGTTACATTTGATGAAAAAGTACAACGTTCAITGATGATTAAGTGGGT
 GTTATCCCTGTCCTTGAGCAAAACCCAGCATCTACAGATGATATGTTTGA
 GGTTGCAGAACGTTAGCACTTGAAGCAGGACTTGTGTAATCAGGCGATA
 ATATCGTATATCGTTGCAAGGTGTTCCCTGTAGGTACAGGTGGAACCTAACACA
 ATGCGTGTTCGTACTGTTAAA

Table 72: Comparative Sequences relating to SAG0941

ATATCGTTATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAACCTAACACA
ATGCGGTGTTCTACTGTTAAA

SEQ ID NO. 7211

STRAIN JM9130013

AAATAACCGCTAAAAATCGTTGCAAC
ACTTGGTCCCTGCGGTAGAAATCCCTGGTGGTAAGAAGTTTGGTGGAGTCTG
GATACCTGGGTGAAAGCCTTGACGTAGAAGCTTCAGCAGAAAAAATTTGCT
CAATTGATTAAGAAGGCTAACGTTTCCCGTTTCAACTTCTCACATGG
AGATCATGCTGAGCAAGGAGCTCGTATGGCTACTGTTTCGTAAGCAGAAAG
AGATTGCAGGACAAAAAGTTGGCTTCCCTCCTTGATACTAAAGGACCTGAA
ATTCGTACAGAACTTTTGAAGATGGTTCAGATTTCCATTTCATATACAAC
AGGTACAAAAATACGCTGCTACTAAGCAAGGTATCAAATCAACTCCAG
AAGTGATTGCATTGAATGTTGCTGGTGGACTTGACATCTTTGATGACGTT
GAAGTTGGTAAAGCAAAATCCTTGTGATGATGGTAAACTAGGTCTTACTGT
GTTTGCAAAAGATAAAGCACTCGTGAATTTGAAGTAGTTGTTGAGAATG
ATGGCCTTATTGGTAAACAAAAAGGTGTAACATCCCTTATACTAAAAAT
CCTTTCCAGCACTTCAGAACCGGATAATGCTGATATCCGTTTGGACT
TGAGCAAGGACTTAACCTTATTGCTATCTCATTTGTACGTACTGCTAAAG
ATGTTAATGAAGTTTCTGCTATTGTGAAGAACTGGCAATGGACATGTT
AAGTTGTTGCTAAAATGAAATCAACAAGGTATCGATAAATATGATGA
GATTATCGAAGCAGCAGATGGTATTATGATGCTCGTGGTATATGGGTA
TCGAAGTCCATTTGAAATGGTTCAGTTTACCAAAAAATGATCATTACT
AAAGTTAATGCAGCTGGTAAAGCAGTTATACAGCAACAATAATGCTTGA
AACAATGACTGATAAACCCAGTGGCAGCTCGTTGCAAGTATCTGATGCT
TCATGCTGTTATTGATGGTACTGATGCTACAATGCTTTCAGGTGAGTCA
GCTAATGGTAAATACCCAGTTGAGTCACTTTCGTAATGGCTACTATTGA
TAAAAATGCTCAAACATTACTCAATGAGTATGGTTCGCTTACACTCATCTG
CAATCCACGTAATAAACAACAACTGATTTATGCACTGCGGTTAAAGAT
GCACCACTCAATGGATATCAAACCTGTTGTCACAACTACTGAAACAGG
TAATACAGCTCGTCCATTTCTAAATCCGTCAGATGCAGACATTTTGG
CTGTTACATTTGATGAAAAAGTACAACGTTTATTGATGATTAACCTGGGGT
GTTATCCCTGCTTCAGACAAACAGCATCTACAGATGATATGTTTGA
GGTTGCAGAACGTTAGcACTTGAAGCAGGACTTGTGAATCAGGCGATA
ATATCGTTATCGTTGCAGGTGTTCCCTGTAGGTACAGGTGGAACCTAACACA
ATGCGGTGTTCTACTGTTAAA

PRETTY of: /biotmp/msa277466.2{*} February 24, 2003 01:44 ..

1 50
msa277466.2{330_090} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT
msa277466.2{330_JM9130013} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT
msa277466.2{330_18RS21} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTtGAATT
msa277466.2{330_2603} atgAATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTtGAATT
msa277466.2{330_A909} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTtGAATT
msa277466.2{330_H36B} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTtGAATT
msa277466.2{330_CJB110} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTtGAATT
msa277466.2{330_COH1} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT
msa277466.2{330_M732} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT
msa277466.2{330_1169NT} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT
msa277466.2{330_M781} ---AATAAAC GCGTAAAAAT CGTTGCAACA CTTGGTCCCTG CGGTaGAATT
Consensus *****

51 100
msa277466.2{330_090} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_JM9130013} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_18RS21} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_2603} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_A909} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_H36B} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_CJB110} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_COH1} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_M732} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_1169NT} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
msa277466.2{330_M781} CCGTGGTGGT AAGAAGTTTGT GTGAGTCTGG ATACTGGGGT GAAAGCCTTG
Consensus *****

101 150
msa277466.2{330_090} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_JM9130013} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_18RS21} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_2603} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_A909} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_H36B} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_CJB110} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_COH1} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_M732} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_1169NT} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
msa277466.2{330_M781} ACGTAGAAGC TTCAGCAGAA AAAATTGCTC AATTGATTAA AGAAGGTGCT
Consensus *****

151 200
msa277466.2{330_090} AACGTTTTCC GTTTCACCTT CTCACATGGA GATCATGCTG AGCAAGGAGC

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_JM9130013}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_18RS21}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_2603}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_A909}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_H36B}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_CJB110}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_COH1}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M732}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_1169NT}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
msa277466.2{330_M781}	AACGTTTTCC	GTTTCAACTT	CTCACATGGA	GATCATGCTG	AGCAAGGAGC
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_JM9130013}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_18RS21}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_2603}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_A909}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_H36B}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_CJB110}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_COH1}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M732}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_1169NT}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
msa277466.2{330_M781}	TCGTATGGCT	ACTGTTTCGTA	AAGCAGAAGA	GATTGCAGGA	CAAAAAGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_JM9130013}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_18RS21}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_2603}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_A909}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_H36B}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_CJB110}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_COH1}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M732}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_1169NT}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
msa277466.2{330_M781}	GCTTCCTCCT	TGATACTAAA	GGACCTGAAA	TTCGTACAGA	ACTTTTTGAA
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_JM9130013}	GATGGTtCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_18RS21}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_2603}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_A909}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_H36B}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_CJB110}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_COH1}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M732}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_1169NT}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
msa277466.2{330_M781}	GATGGTgCAG	ATTTCcATTC	ATATACAACA	GGTACaAAT	TACGTGTTGC
Consensus	*****_***	*****	*****	*****_***	*****
msa277466.2{330_090}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_JM9130013}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_18RS21}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_2603}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_A909}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_H36B}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_CJB110}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_COH1}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M732}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_1169NT}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
msa277466.2{330_M781}	TACTAAGCAA	GGTATCAAAAT	CAACTCCAGA	AGTGATTGCA	TTGAATGTTG
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
Consensus	*****	*****	*****	*****	*****
msa277466.2{330_090}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_JM9130013}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_18RS21}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_2603}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_A909}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_H36B}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_CJB110}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_COH1}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M732}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_1169NT}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
msa277466.2{330_M781}	CTGGTGGACT	TGACATCITT	GATGACGTTG	AAGTTGGTAA	GCAAATCCTT
Consensus	*****	*****	*****	*****	*****

451

500

Table 72: Comparative Sequences relating to SAG0941

msa277466.2{330_090}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_JM9130013}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_18RS21}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_2603}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_A909}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_H36B}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_CJB110}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_COH1}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_M732}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_1169NT}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
msa277466.2{330_M781}	GTTGATGATG	GTAAACTAGG	TCCTACTGTG	TTTGCAAAG	ATAAAGACAC
Consensus	*****	*****	*****	*****	*****

	501			550	
msa277466.2{330_090}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_JM9130013}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_18RS21}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_2603}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_A909}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_H36B}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_CJB110}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_COH1}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M732}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_1169NT}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
msa277466.2{330_M781}	TCGTGAATTT	GAAGTAGTTG	TTGAGAAATGA	TGGCCTTATT	GGTAAACAAA
Consensus	*****	*****	*****	*****	*****

	551			600	
msa277466.2{330_090}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_JM9130013}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_18RS21}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_2603}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_A909}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_H36B}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_CJB110}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_COH1}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_M732}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_1169NT}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
msa277466.2{330_M781}	AAGGTGTAAA	CATCCCTTAT	ACTAAAATTC	CITTCCCAGC	ACTTGCAGAA
Consensus	*****	*****	*****	*****	*****

	601			650	
msa277466.2{330_090}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_JM9130013}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_18RS21}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_2603}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_A909}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_H36B}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_CJB110}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GaaCAAGGAC	TTAACTTTAT
msa277466.2{330_COH1}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_M732}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_1169NT}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
msa277466.2{330_M781}	CGCGATAATG	CTGATATCCG	TTTTGGACTT	GAgCAAGGAC	TTAACTTTAT
Consensus	*****	*****	*****	**_*****	*****

	651			700	
msa277466.2{330_090}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_JM9130013}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_18RS21}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_2603}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_A909}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_H36B}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_CJB110}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_COH1}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_M732}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_1169NT}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
msa277466.2{330_M781}	TGCTATCTCA	TTTGTACGTA	CTGCTAAAGA	TGTTAATGAA	GTTGCGTGCTA
Consensus	*****	*****	*****	*****	*****

	701			750	
msa277466.2{330_090}	TTTGTGAAGA	AACTGGcaAT	GGACatGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_JM9130013}	TTTGTGAAGA	AACTGGcaAT	GGACatGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_18RS21}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_2603}	TTTGTGAAGA	AACTGGsmAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_A909}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_H36B}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_CJB110}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_COH1}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M732}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_1169NT}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
msa277466.2{330_M781}	TTTGTGAAGA	AACTGGcaAT	GGACAcGTIA	AGTTGTTTGC	TAAAATTGAA
Consensus	*****	*****	*****	*****	*****

Table 72: Comparative Sequences relating to SAG0941

	1051			1100	
msa277466.2{330_090}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_JM9130013}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_18RS21}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_2603}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_A909}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_H36B}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_CJB110}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_COH1}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_M732}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_1169NT}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
msa277466.2{330_M781}	GAGTCAGTTC	GTACAATGGC	TACTATTGAT	AAAAATGCTC	AAACATTACT
Consensus	*****	*****	*****	*****	*****

	1101			1150	
msa277466.2{330_090}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_JM9130013}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_18RS21}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_2603}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_A909}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_H36B}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_CJB110}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_COH1}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_M732}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_1169NT}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
msa277466.2{330_M781}	CAATGAGTAT	GGTCGcTTAG	ACTCATCTGC	ATTCCCACGT	AATAACAAAA
Consensus	*****	*****	*****	*****	*****

	1151			1200	
msa277466.2{330_090}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_JM9130013}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_18RS21}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_2603}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_A909}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_H36B}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_CJB110}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_COH1}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_M732}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_1169NT}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
msa277466.2{330_M781}	CTGATGTTAT	TGCATCTGCG	GTTAAAGATG	CAACACACTC	AATGGATATC
Consensus	*****	*****	*****	*****	*****

	1201			1250	
msa277466.2{330_090}	AAACTTGTTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_JM9130013}	AAACTTGTTG	TgACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_18RS21}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_2603}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_A909}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_H36B}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_CJB110}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_COH1}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_M732}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_1169NT}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
msa277466.2{330_M781}	AAACTTGTTG	TaACAATTAC	TGAAACAGGT	AATACAGCTC	GTGCCATTTC
Consensus	*****	*-*****	*****	*****	*****

	1251			1300	
msa277466.2{330_090}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_JM9130013}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_18RS21}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_2603}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_A909}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_H36B}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_CJB110}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_COH1}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_M732}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_1169NT}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
msa277466.2{330_M781}	TAAaTTCCGT	CCAGATGCAG	ACATTTTGGC	TGTTACATTT	GATGAAAAAG
Consensus	***-*****	*****	*****	*****	*****

	1301			1350	
msa277466.2{330_090}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_JM9130013}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_18RS21}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_2603}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_A909}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_H36B}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_CJB110}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_COH1}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_M732}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_1169NT}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC
msa277466.2{330_M781}	TACAACGTTT	ATTGATGATT	AAC TGGGGT G	TTATCCCTGT	CCTTGCAGAC

Table 72: Comparative Sequences relating to SAG0941

Consensus	*****	*****	*****	*****	*****
	1351				.1400
msa277466.2{330_090}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_JM9130013}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_18RS21}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_2603}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_A909}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_H36B}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_CJB110}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_COH1}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M732}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_1169NT}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
msa277466.2{330_M781}	AAACCAGCAT	CTACAGATGA	TATGTTTGAG	GTTGCAGAAC	GTGTAGCACT
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa277466.2{330_090}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_JM9130013}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_18RS21}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_2603}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_A909}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_H36B}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_CJB110}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_COH1}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M732}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_1169NT}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
msa277466.2{330_M781}	TGAAGCAGGA	cTTGTTGAAT	CAGGCGATAA	TATCGTTATC	GTTGCAGGTG
Consensus	*****	-*****	*****	*****	*****
	1451				1500
msa277466.2{330_090}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_JM9130013}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_18RS21}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_2603}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_A909}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_H36B}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_CJB110}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_COH1}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M732}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_1169NT}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
msa277466.2{330_M781}	TTCCCTGTAGG	TACAGGTGGA	ACTAACACAA	TGCGTGTTCG	TACTGTTAAA
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7212

STRAIN 2603 frame: 1

MNKRVKIVATLGPVAVFRGGKKGFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHG
DHAEQGARMATVRKAEIAGQKVGFLLDITKGPPIRTELFDGADFHSTYTTGTLKLRVATKQ
GIKSTPEVIALNVAGGLDIFDDVEVKGQILVDDGKLGTLVFAKDKDTRFEVTVVENDGLI
GKQKGVNIPTTKIPFPALAEARNADIRFGLAQGLNFIAISFVRTAKDVNEVRAICEETGX
GHVKLFAKIENQGGIDNIDEIEAADGIMIARGDMGIEVPPFEMVVPVYQKMIITKVNAAAGK
AVITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATID
KNAQTLLNEYGRLDSSAFPRNNKTDVIAVAVKDATHSMDIKLVVTTITETGNTARAIKFRP
PDADILAVTFDEKVRQSLMINWGVIPVLADKPASTDMMFEVAERVALEAGFVESGDNIIV
VAGVPGTGGTNTMRVRTVK

SEQ ID NO. 7213

STRAIN 090 frame: 1

NKRVKIVATLGPVAVFRGGKKGFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEIAGQKVGFLLDITKGPPIRTELFDGSDFHSTYTTGTLRVLATKQG
IKSTPEVIALNVAGGLDIFDDVEVKGQILVDDGKLGTLVFAKDKDTRFEVTVVENDGLIG
KQKGVNIPTTKIPFPALAEARNADIRFGLAQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQGGIDNIDEIEAADGIMIARGDMGIEVPPFEMVVPVYQKMIITKVNAAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIAVAVKDATHSMDIKLVVTTITETGNTARAIKFRP
DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDMMFEVAERVALEAGFVESGDNIIV
AGVPGTGGTNTMRVRTVK

SEQ ID NO. 7214

STRAIN A909 frame: 1

NKRVKIVATLGPVAVFRGGKKGFGESGYWGESLDVEASAEDIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEIAGQKVGFLLDITKGPPIRTELFDGADFHSTYTTGTLKLRVATKQG
GIKSTPEVIALNVAGGLDIFDDVEVKGQILVDDGKLGTLVFAKDKDTRFEVTVVENDGLIG
KQKGVNIPTTKIPFPALAEARNADIRFGLAQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQGGIDNIDEIEAADGIMIARGDMGIEVPPFEMVVPVYQKMIITKVNAAAGKA
VITATNMLETMTDKPRATRSEVSDVFNAVIDGTDATMLSGESANGKYPVESVRTMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIAVAVKDATHSMDIKLVVTTITETGNTARAIKFRP
DADILAVTFDEKVRQSLMINWGVIPVLADKPASTDMMFEVAERVALEAGFVESGDNIIV
AGVPGTGGTNTMRVRTVK

SEQ ID NO. 7215

STRAIN H36B frame: 1

Table 72: Comparative Sequences relating to SAG0941

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7216

STRAIN 18RS21 frame: 1

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7217

STRAIN M732 frame: 1

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7218

STRAIN COH1 frame: 1

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7219

STRAIN M781 frame: 1

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7220

STRAIN CJB110 frame: 1

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

SEQ ID NO. 7221

STRAIN 1169NT frame: 1

NKRVKIVATLGP... HAEQGMATVRK... I KSTPEVIALNVAGGLD... KQKGVNI PYTKI... HVKLFAKIENQQG... VITATNMLETMT... NAQTLLENYGR... DADILLAVTFDEK... AGVPVGTGGTNTMRVRTVK

Table 72: Comparative Sequences relating to SAG0941

SEQ ID NO. 7222

STRAIN JM9130013 frame: 1

NKRVKIVATLGPVAVFRGGKFKFGESGYWGESLDVEASAEKIAQLIKEGANVFRFNFSHGD
HAEQGARMATVRKAEEIAGQKVGFLLDTKGPEIRTELFEDGSDPHSYTTCTKLRVATKQG
IKSTPEVIALNVAGGLDIFDDVEVGKQILVDDGKLGTLVFAKDKDTREFEVVVENDGLIG
KQKGVNIPYTKIPFPALAEARDNADIRFGLGQGLNFIAISFVRTAKDVNEVRAICEETGNG
HVKLFAKIENQOQIDNIDEIIEAADGIMILARGDMGIEVFPFEMVVPYQKMIITKVNAAAGKA
VITATNMLETMTDKPRATRSEVSDVFNVAIDGTDATMLSGESANGKYPVESVTRMATIDK
NAQTLLNEYGRLDSSAFPRNNKTDVIAAVKDATHSMDIKLWVTITETGNTARAISKFRP
DADILAVTFDEKVRSLMINWGVIPVLADKPASTDDMFEVAERVALEAGLVESGDNIIVIV
AGVPVGTGGTNTMRVRTVK

PRETTY of: /biotmp/msa277662.2{*} February 24, 2003 01:49 ..

1 50
msa277662.2{330_18RS21} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_A909} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_CJB110} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_H36B} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_1169NT} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_COH1} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_M732} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_M781} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_JM9130013} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_090} -NKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
msa277662.2{330_2603} mNKRVKIVAT LGPAVEFRGG KKFGESEGYWG ESLDVEASAE KIAQLIKEGA
Consensus *****

51 100
msa277662.2{330_18RS21} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_A909} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_CJB110} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_H36B} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_1169NT} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_COH1} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_M732} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_M781} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_JM9130013} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_090} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
msa277662.2{330_2603} NVFRFNFSHG DHAEQGARMA TVRKAEEIAG QKVGFLLDTK GPEIRTELFEE
Consensus *****

101 150
msa277662.2{330_18RS21} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_A909} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_CJB110} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_H36B} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_1169NT} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_COH1} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_M732} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_M781} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_JM9130013} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_090} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
msa277662.2{330_2603} DGaDFHSYTT GtKLRVATKQ GIKSTPEVIA LNVAGGLDIF DDVEVGKQIL
Consensus **-***** **-***** *****

151 200
msa277662.2{330_18RS21} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_A909} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_CJB110} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_H36B} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_1169NT} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_COH1} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_M732} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_M781} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_JM9130013} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_090} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
msa277662.2{330_2603} VDDGKLGTLV FAKDKDTREF EVVVENDGLI GKQKGVNIPY TKIPFPALAE
Consensus *****

201 250
msa277662.2{330_18RS21} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_A909} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_CJB110} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_H36B} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_1169NT} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_COH1} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_M732} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_M781} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_JM9130013} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_090} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGn GHVKLFAKIE
msa277662.2{330_2603} RDNADIRFGL EQGLNFIAIS FVRTAKDVNE VRAICEETGx GHVKLFAKIE
Consensus *****

Table 72: Comparative Sequences relating to SAG0941

	251				300
msa277662.2{330_18RS21}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_A909}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_CJB110}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_H36B}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_1169NT}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_COH1}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_M732}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_M781}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_JM9130013}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_090}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
msa277662.2{330_2603}	NQQGIDNIDE	IIEAADGIMI	ARGDMGIEVP	FEMVVPVYQKM	IITKVNAAGK
Consensus	*****	*****	*****	*****	*****
	301				350
msa277662.2{330_18RS21}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_A909}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_CJB110}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_H36B}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_1169NT}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_COH1}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M732}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_M781}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_JM9130013}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_090}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
msa277662.2{330_2603}	AVITATNMLE	TMTDKPRATR	SEVSDVFNAV	IDGTDATMLS	GESANGKYPV
Consensus	*****	*****	*****	*****	*****
	351				400
msa277662.2{330_18RS21}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_A909}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_CJB110}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_H36B}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_1169NT}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_COH1}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_M732}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_M781}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_JM9130013}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_090}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
msa277662.2{330_2603}	ESVRTMATID	KNAQTLLENEY	GRLDSSAFPR	NNKTDVIAASA	VKDATHSMIDI
Consensus	*****	*****	*****	*****	*****
	401				450
msa277662.2{330_18RS21}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_A909}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_CJB110}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_H36B}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_1169NT}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_COH1}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_M732}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_M781}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_JM9130013}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_090}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
msa277662.2{330_2603}	KLVVTTITETG	NTARAIKFR	PDADILAVTF	DEKVQRSLMI	NWGVIPVLAD
Consensus	*****	*****	*****	*****	*****
	451				500
msa277662.2{330_18RS21}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_A909}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_CJB110}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_H36B}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_1169NT}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_COH1}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_M732}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_M781}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_JM9130013}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_090}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
msa277662.2{330_2603}	KPASTDDMFE	VAERVALEAG	FVESGDNIVI	VAGVPVGTGG	TNIMRVRTVK
Consensus	*****	*****	*****	*****	*****

Table 73: Comparative Sequences relating to SAG0981

SEQ ID NO. 7301

STRAIN 2603

TTGTCGTATAAATAGACAAAAAGGTGGTGATATTTATGTATTTAGCATTAAATCGGTGAT
ATCATTAAATCAAACAGATACTTGAAACGTGAAACCTTCCAAACAGTCTTTTCAGCAACTA
ATGACCGAAGCTATCTGATGATATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCT
GGTGATGAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCAT
ATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTACAGGAAACATTATA
ACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTCCCTACTGGCATGCTCGC
TCAGCTATTAAATCATATACATGATAAAAATGATTATGGAACAGTTCAAGTAGCTATTTCG
CTTGATGATGAAGACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAAGCTGGTGAT
TTTATCAAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAA
GATAATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATTGAACCT
AGTGGCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATTTACTTAAGAACGAGAACA
CAGGCAGCCGATCTATTAGTTAAAGTTGCACCTCAAACCTAAAGGGGAAGCTATGATTTT

SEQ ID NO. 7302

STRAIN 090

TCTGCTATAAATAGACAAAAAGGTGGTGATATTTATGTATTT
AGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTGAAACGTGAAA
CTTTCCAAACAGTCTTTTCAGCAAATAATGACCGAAGCTATCTGATGATAT
GGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTTCA
AGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATATTTC
AACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTACAGGAAAC
ATTATAACATCCATCAATTTAAATGAAAGTATCGGTGCTGATGGTCTCGC
CTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAAATGATT
ATGGAACAGTTCAAGTAGCTATTTCGCTTGATGATGAAGACCAAAACCTT
GAATTAACACTAAATAGTCTCATTTCAAGCTGGTGATTTTATCAAGTCAA
ATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGATA
ATTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATATT
GAACCTAGTGGCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATTTA
CTTAAGAACGAGAACAACAGGCAGCCGATCTATTAGTTAAAGTTGCACCT
AAACTAAAGGGGAAGCTATGATTTT

SEQ ID NO. 7303

STRAIN A909

TCTGCTATAAATAGACAAAAAGGTGGTGATATTTATGTATTT
TTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTGAAACGTGA
AACTTTCCAAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTGATGAT
ATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGATGAATTT
CAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGACCATAT
TCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTACAGGAA
ACATTTATAACATCCATCAATTCAAATGAAAGTATCGGTGCTGATGGTCTC
GCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAAAAATGA
TTATGGAACAGTTCAAGTAGCTATTTCGCTTGATGATGAAGACCAAAAC
TTGAATTAACACTAAATAGTCTCATTTCAAGCTGGTGATTTTATCAAGTCA
AAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACTTCAAGA
TAATTTATCAAGAACAAATTTCAACATCAAAAGTTAGCCCAACTGGAAAATA
TTGAACCTAGTGGCTGACTAAACGCTTAAAGCAAGCGGTCTGAAGATT
TACTTAAGAACGAGAACAACAGGCAGCCGATCTATTAGTTAAAGTTGCAC
TCAAACCTAAAGGGGAAGCTATGATTTT

SEQ ID NO. 7304

STRAIN H36B

TCTGCTATAAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTA
CAGGAAACATTTAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCTCGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTCGCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAAGCTGGTGATTTTATC
AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAAATTTCAAGAACAAATTTCAACATCAAAAGTTAGCCCAACTGG
AAAATATTGAACCTAGTGGCTGACTAAACGCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAGAACGAGAACAACAGGCAGCCGATCTATTAGTTAAAG
TTGCACCTCAAACCTAAAGGGGAAGCTATGATTTT

SEQ ID NO. 7305

STRAIN 18RS21

TCTGCTATAAATAGACAAAAAGGTGGTGATATTT
ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTGA
ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAAGCTATCTG
ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTATTGAAACCATCAAAAAGGTATTTCAAATTATTGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGTA
CAGGAAACATTTAACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCTCGCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATAA
AAATGATTATGGAACAGTTCAAGTAGCTATTTCGCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAAGCTGGTGATTTTATC
AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT

Table 73: Comparative Sequences relating to SAG0981

TCAAGATAATTATCAAGAACAAATTTCAACATCAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCCTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7306

STRAIN M732

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAAACAATCAAAGGTTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTATTATTTAT
 CAAGTCAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAGTTAGCCCAACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 GTTGCCTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7307

STRAIN COH1

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 TATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTG
 AACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCT
 GATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 TGAATTTCAAGCTTTATTTGAAACAATCAAAGGTTATTTCAAATTTATTG
 ACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 ACAGGAAACATTATAACATCCATCAATCAAATGAAAGTATCGGTGCTGA
 TGGTCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 CAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTATTATTTAT
 CAAGTCAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATAC
 TTCAAGATAATTATCAAGAACAAATTTCAACATCAAAGTTAGCCCAACTG
 GAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCT
 GAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 GTTGCCTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7308

STRAIN M781

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG
 ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGA
 GAATTTCAAGCTTTATTTGAAACAATCAAAGGTTATTTCAAATTTATTGA
 CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCGGT
 CAGGAAACATTATAACATCCATCAATCAAATGAAAGTATCGGTGCTGAT
 GGTCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGATA
 AATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGAC
 AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTATTATTTATC
 AAGTCAAATGGACTACAAACCAATTTCAAATGCTTGAGCACTTAATACT
 TCAAGATAATTATCAAGAACAAATTTCAACATCAAAGTTAGCCCAACTGG
 AAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGTCTG
 AAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAAAG
 TTGCCTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7309

STRAIN CJB110

TCTGCTATAATAGACAAAAAGGTGGTGGTA
 TTTATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACT
 TGAACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTAT
 CTGATGTATATGGTGAAGAGCTGATTTCTCTATTCACTATTACAGCTGGT
 GATGAATTTCAAGCTTTATTTGAAACCATCAAAGGTTATTTCAAATTTAT
 TGACCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGCCCTCG
 GTACAGGAAACATTATAACATCCATCAATCAAATGAAAGTATCGGTGCT
 GATGGTCTGCCTACTGGCATGCTCGCTCAGCTATTAAATCATATACATGA
 TAAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAG
 ACCAAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTATTATTT
 ATCAAGTCAAATGGACTACTAACCAATTTCAAATGCTTGAGCACTTAAT
 ACTTCAAGATAATTATCAAGAACAAATTTCAACATCAAAGTTAGCCCAAC
 TGGAAAATATTGAACCTAGTGCCTGACTAAACGCCCTAAAGCAAGCGGT
 CTGAAGATTTACTTAAGAACGAGAACACAGGCAGCCGATCTATTAGTTAA
 AAGTTGCCTCAAACATAAGGGGGAAGCTATGATTTTC

SEQ ID NO. 7310

STRAIN JM9130013

TCTGCTATAATAGACAAAAAGGTGGTGATATT
 ATGTATTTAGCATTAAATCGGTGATATCATTAAATCAAACAGATACTTGA
 ACGTGAAACTTTCCAACAGTCTTTTCAGCAACTAATGACCGAACTATCTG

Table 73: Comparative Sequences relating to SAG0981

ATGTATATGGTGAAGAGCTGATTTCTCCATTCACTATTACAGCTGGTGAT
GAATTTCAAGCTTTAATGAAAACCAACAAAAAGGTATTTCAAATTTATGA
CCATATTCAACTAGCTCTAAAACCTGTTAATGTAAGGTTCCGGCTCGGTA
CAGGAAACATTTAATACATCCATCAATTCAAATGAAAGTATCGGTGCTGAT
GGTCTCGCTACTGCGCATGCTCGCTCAGCTATTAATCATATACATGATAA
AAAATGATTATGGAACAGTTCAAGTAGCTATTTGCCTTGATGATGAAGACC
AAAACCTTGAATTAACACTAAATAGTCTCATTTCAGCTGGTGATTTTATC
AAGTCAAATGGACTACAAACCATTTTCAAATGCTTGAGCACTTAATACT
TCAAGATAATTTCAAGAACAAATTTCAACATCAAAGTTAGCCCACTGG
AAAATATTGAACCTAGTGGCTGACTAAAACGCTTAAAGCAAGCGGTCTG
AAGATTTACTTAAAGACGAGAACACAGGCGAGCCGATCTATTAGTTAAAG
TTGCACTCAAACCTAAAGGGGAGCTATGATTTT

PRETTY of: /biotmp/msa31912.2{*} February 18, 2003 08:19 ..

1 50
msa31912.2{338_18RS21} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_2603} ttgTCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_A909} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_H36B} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_JM9130013} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_COH1} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_M732} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_M781} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_090} ---TCTGCTA TAATAGACAA AAAGGTGGTG aTATTTATGT ATTTAGCATT
msa31912.2{338_CJB110} ---TCTGCTA TAATAGACAA AAAGGTGGTG gTATTTATGT ATTTAGCATT
Consensus ***** -*****

51 100
msa31912.2{338_18RS21} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_2603} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_A909} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_H36B} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_JM9130013} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_COH1} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_M732} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_M781} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_090} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
msa31912.2{338_CJB110} AATCGGTGAT ATCATTAAAT CAAAACAGAT ACTTGAACGT GAAACTTTCC
Consensus *****

101 150
msa31912.2{338_18RS21} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_2603} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_A909} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_H36B} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_JM9130013} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_COH1} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_M732} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_M781} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_090} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
msa31912.2{338_CJB110} AACAGTCTTT TCAGCAACTA ATGACCGAAC TATCTGATGT ATATGGTGAA
Consensus *****

151 200
msa31912.2{338_18RS21} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_2603} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_A909} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_H36B} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_JM9130013} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_COH1} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_M732} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_M781} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_090} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
msa31912.2{338_CJB110} GAGCTGATTT CTCcATTcAC TATTACAGCT GGTGATGAAT TTCaAGCTTT
Consensus *****

201 250
msa31912.2{338_18RS21} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_2603} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_A909} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_H36B} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_JM9130013} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_COH1} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_M732} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_M781} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_090} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
msa31912.2{338_CJB110} AITGAAACcA TCAAAAAGG TATTTCAAAT TATTGACCAT ATTCaACTAG
Consensus *****

251 300
msa31912.2{338_18RS21} CTCTAAaACC TGTTAAATGTA AGGTTcGGCC TCGGTACAGG AAACATTATA
msa31912.2{338_2603} CTCTAAaACC TGTTAAATGTA AGGTTcGGCC TCGGTACAGG AAACATTATA

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_A909}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_H36B}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_JM9130013}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_COH1}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_M732}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_M781}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_090}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
msa31912.2{338_CJB110}	CTCTAAAACC	TGTTAATGTA	AGGTTCGGCC	TCGGTACAGG	AAACATTATA
Consensus	*****	*****	*****	*****	*****
301					
msa31912.2{338_18RS21}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_2603}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_A909}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_H36B}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_JM9130013}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_COH1}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_M732}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_M781}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_090}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
msa31912.2{338_CJB110}	ACATCCATCA	ATTCAAATGA	AAGTATCGGT	GCTGATGGTC	CTGCCTACTG
Consensus	*****	***-*****	*****	*****	*****
351					
msa31912.2{338_18RS21}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_2603}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_A909}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_H36B}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_JM9130013}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_COH1}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_M732}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_M781}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_090}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
msa31912.2{338_CJB110}	GCATGCTCGC	TCAGCTATTA	ATCATATACA	TGATAAAAAT	GATTATGGAA
Consensus	*****	*****	*****	*****	*****
401					
msa31912.2{338_18RS21}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_2603}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_A909}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_H36B}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_JM9130013}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_COH1}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_M732}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_M781}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_090}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
msa31912.2{338_CJB110}	CAGTTC AAGT	AGCTATTGTC	CTTGATGATG	AAGACCAAAA	CCTTGAATTA
Consensus	*****	*****	*****	*****	*****
451					
msa31912.2{338_18RS21}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_2603}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_A909}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_H36B}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_JM9130013}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_COH1}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_M732}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_M781}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_090}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
msa31912.2{338_CJB110}	ACACTAAATA	GTCTCATTTT	AGCTGGTGAT	TTTATCAAGT	CAAAATGGAC
Consensus	*****	*****	*****	*****	*****
501					
msa31912.2{338_18RS21}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_2603}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_A909}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_H36B}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_JM9130013}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_COH1}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_M732}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_M781}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_090}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
msa31912.2{338_CJB110}	TACaAACCAT	TTTCAAATGC	TTGAGCAGT	AATACTTCAA	GATAAATTATC
Consensus	***-*****	*****	*****	*****	*****
551					
msa31912.2{338_18RS21}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_2603}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_A909}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_H36B}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_JM9130013}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_COH1}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_M732}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT

Table 73: Comparative Sequences relating to SAG0981

msa31912.2{338_M781}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_090}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
msa31912.2{338_CJB110}	AAGAACAATT	TCAACATCAA	AAGTTAGCCC	AACTGGAAAA	TATTGAACCT
Consensus	*****	*****	*****	*****	*****
601					
msa31912.2{338_18RS21}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_2603}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_A909}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_H36B}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_JM9130013}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_COH1}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M732}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_M781}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_090}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
msa31912.2{338_CJB110}	AGTGCGCTGA	CTAAACGCCT	TAAAGCAAGC	GGTCTGAAGA	TTTACTTAAG
Consensus	*****	*****	*****	*****	*****
651					
msa31912.2{338_18RS21}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_2603}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_A909}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_H36B}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_JM9130013}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_COH1}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M732}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_M781}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_090}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
msa31912.2{338_CJB110}	AACGAGAACA	CAGGCAGCCG	ATCTATTAGT	TAAAAGTTGC	ACTCAAACCTA
Consensus	*****	*****	*****	*****	*****
701					
msa31912.2{338_18RS21}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_2603}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_A909}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_H36B}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_JM9130013}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_COH1}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_M732}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_M781}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_090}	AAGGGGAAG	CTATGATTTC			
msa31912.2{338_CJB110}	AAGGGGAAG	CTATGATTTC			
Consensus	*****	*****			

SEQ ID NO. 7311
 STRAIN 2603 frame: 1
 LSAIDKVVIFMYLALIGDIINSEQILERETFQOSFQQLMTELSDVYGEELISPFITITA
 GDEFQALLKPKSKVVFQIIDHIQLALKPVNVRFLGTGNIITSINSNESIGADGPAYWHAR
 SAINHIHDKNDYGTVQVAICLDDDEDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLIILQD
 NYQEQQFHQKLAQLENIEPSALTKRKLKASGLKIYLRTRTQAADLLVKSCTQTCKGGSYDF

SEQ ID NO. 7312
 STRAIN 090 frame: 1
 SAIIDKVVIFMYLALIGDIINSEQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKPKSKVVFQIIDHIQLALKPVNVRFLGTGNIITSINLNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDDEDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLIILQD
 NYQEQQFHQKLAQLENIEPSALTKRKLKASGLKIYLRTRTQAADLLVKSCTQTCKGGSYDF

SEQ ID NO. 7313
 STRAIN A909 frame: 1
 SAIIDKVVIFMYLALIGDIINSEQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKPKSKVVFQIIDHIQLALKPVNVRFLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDDEDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLIILQD
 NYQEQQFHQKLAQLENIEPSALTKRKLKASGLKIYLRTRTQAADLLVKSCTQTCKGGSYDF

SEQ ID NO. 7314
 STRAIN H36B frame: 1
 SAIIDKVVIFMYLALIGDIINSEQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKPKSKVVFQIIDHIQLALKPVNVRFLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDDEDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLIILQD
 NYQEQQFHQKLAQLENIEPSALTKRKLKASGLKIYLRTRTQAADLLVKSCTQTCKGGSYDF

SEQ ID NO. 7315
 STRAIN 18RS21 frame: 1
 SAIIDKVVIFMYLALIGDIINSEQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
 DEFQALLKPKSKVVFQIIDHIQLALKPVNVRFLGTGNIITSINSNESIGADGPAYWHARS
 AINHIHDKNDYGTVQVAICLDDDEDQNLLETLNLSISAGDFIKSKWTTNHFQMLEHLIILQD
 NYQEQQFHQKLAQLENIEPSALTKRKLKASGLKIYLRTRTQAADLLVKSCTQTCKGGSYDF

SEQ ID NO. 7316
 STRAIN M732 frame: 1
 SAIIDKVVIFMYLALIGDIINSEQILERETFQOSFQQLMTELSDVYGEELISPFITITAG

Table 73: Comparative Sequences relating to SAG0981

DEFQALLKQSKKVFQI IDHIQLALKPVNVRFGLGTGNI ITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDDEDQNLLELTLSNLSISAGDFIKSKWTTNHFQMLEHLIILQD
NYQEQQFHQKLAQLENI EPSALTKRKLKASGLKI YLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7317

STRAIN COHI frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
DEFQALLKQSKKVFQI IDHIQLALKPVNVRFGLGTGNI ITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDDEDQNLLELTLSNLSISAGDFIKSKWTTNHFQMLEHLIILQD
NYQEQQFHQKLAQLENI EPSALTKRKLKASGLKI YLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7318

STRAIN M781 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
DEFQALLKQSKKVFQI IDHIQLALKPVNVRFGLGTGNI ITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDDEDQNLLELTLSNLSISAGDFIKSKWTTNHFQMLEHLIILQD
NYQEQQFHQKLAQLENI EPSALTKRKLKASGLKI YLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7319

STRAIN CJB110 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQOSFQQLMTELSDVYGEELISLFTITITAG
DEFQALLKQSKKVFQI IDHIQLALKPVNVRFGLGTGNI ITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDDEDQNLLELTLSNLSISAGDFIKSKWTTNHFQMLEHLIILQD
NYQEQQFHQKLAQLENI EPSALTKRKLKASGLKI YLRTRTQAADLLVKSCQTQKGGSYDF

SEQ ID NO. 7320

STRAIN JM9130013 frame: 1

SAIIDKKVVI FMYLALIGDI INSKQILERETFQOSFQQLMTELSDVYGEELISPFITITAG
DEFQALLKQSKKVFQI IDHIQLALKPVNVRFGLGTGNI ITSINSNESIGADGPAYWHARS
AINHIHDKNDYGTVQVAICLDDDEDQNLLELTLSNLSISAGDFIKSKWTTNHFQMLEHLIILQD
NYQEQQFHQKLAQLENI EPSALTKRKLKASGLKI YLRTRTQAADLLVKSCQTQKGGSYDF

PRETTY of: /biotmp/msa32053.2{*} February 18, 2003 08:25 ..

msa32053.2{338_18RS21} 1 ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE 50
msa32053.2{338_2603} lSAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_A909} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_CJB110} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_COH1} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_H36B} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_JM9130013} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_M732} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_M781} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
msa32053.2{338_090} ~SAIIDKKVV IFMYLALIGD I INSKQILER ETFQOSFQQL MTELSDVYGE
Consensus ***** -***** ***** ***** *****

msa32053.2{338_18RS21} 51 ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I 100
msa32053.2{338_2603} ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_A909} ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_CJB110} ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_COH1} ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_H36B} ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_JM9130013} ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_M732} ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_M781} ELISpFTITA GDEFQALLKq SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
msa32053.2{338_090} ELISpFTITA GDEFQALLKp SKKVFQIIDH IQLALKPVNV RFGLGTGNI I
Consensus ****-**** *****- ***** ***** *****

msa32053.2{338_18RS21} 101 TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL 150
msa32053.2{338_2603} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_A909} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_CJB110} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_COH1} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_H36B} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_JM9130013} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_M732} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_M781} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
msa32053.2{338_090} TSINsNESIG ADGPAYWHAR SAINHIHDKN DYGTVQVAIC LDDDEDQNLLEL
Consensus ****-**** ***** ***** ***** *****

msa32053.2{338_18RS21} 151 TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP 200
msa32053.2{338_2603} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_A909} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_CJB110} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_COH1} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_H36B} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_JM9130013} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_M732} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP
msa32053.2{338_M781} TLNSLISAGD FIKSKWTTNH FQMLEHLIILQ DNYQEQQFHQ KLAQLENI EP

Table 73: Comparative Sequences relating to SAG0981

msa32053.2{338_090}	TLNSLISAGD	FIKSKWTTNH	FQMLEHLILQ	DNYQEQFQHQ	KLAQLENIEP
Consensus	*****	*****	*****	*****	*****
	201			240	
msa32053.2{338_18RS21}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_2603}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_A909}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_CJB110}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_COH1}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_H36B}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_JM9130013}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M732}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_M781}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
msa32053.2{338_090}	SALTKRLKAS	GLKIYLRTRT	QAADLLVKSC	TQTKGGSYDF	
Consensus	*****	*****	*****	*****	

Table 74: Comparative Sequences relating to SAG1572

SEQ ID NO. 7401

STRAIN 2603

ATGGAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACTCTAT
CTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGGATTTTA
AGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCAC
TTTGATATTACTACTAAACAAATTAGTTTTACCGAACACAATGCTTACGATAAAATCTCT
GGTTAATTGATTTGTTAAAAGAAGGGAAATCTTAGCCCAAGTATCTGATGCAGGAATG
CCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGGTTTAGCT
CCACAACCTCATATTTTTTATGGCTTCTTACCTCGTAAGAAAGGTCAACAAATAACTTTC
TTTGAACAAGCAAGATTACCTGAAACACAATCTTTTATGAGTCACCGTTTCGAGTC
TCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGC
GAATTTGACGAACTCTATGAAGAGTATCAAAGAGGAAACCAATTAGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATATTGTTGATGGTAAAGAGAGATACC
GAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGTAAAAGAATATATCGCT
AATGGTGATAAAACTAATCAAGCGATAAAAAAAGTAGCAAAGAATTTAATCTCAATAGA
CAAGAACTCTATGCTAGTTCCATGATTTA

SEQ ID NO. 7402

STRAIN 090

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATTACGGGACACT
CTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTG
CCATTAGGATTTTAAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGA
AATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAACAATTAG
TTTTACGAAACACAATGCTTACGATAAAATCTCTGGTTAATTGATTTGT
TAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCT
ATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGAT
CCCGTCTGATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCG
CTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCGGCT
AGAAAAGGTCAACAATAACTTTTTTGAACAAGAAAGATTACCCCTG
AACACAATCTTTTATGAGTCAACCGTTTCGAGTCTCTGATACGCTAAAAC
ACATGAAGAGATTACGGAGATCGCCAAGTTGTTTTAGTACGGAAATTG
ACGAACTCTATGAAGAGTATCAAAGAGGAAACCAATTAGTCAACTTTTAGG
GCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATATTGTTGATG
GTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTA
GTATTAGTAA

SEQ ID NO. 7403

STRAIN A909

AGTTCAAAAAAGTTTTAAATCAAATATACATTACGGAACTCTATCTAG
TCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGCCATTAGG
ATTTTAAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAAATACGGG
ACTTTTACTCAAGCACTTTGATATTACTACTAAACAATTAGTTTTACAG
AAGACAATGCTTACGATAAAATCTCTGGTTAATTGATTTGTTAAAAGAA
GGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTTCTGA
CCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCAGTTG
TATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTCAGG
TTAGCTCCACAACCTCATATTTTTTATGGCTTCTTACCACGTAAGAAAGG
TCAACAATAACTTTCTTTTGAACAAGCAAGATTACCCCTGAAACACAAA
TCTTTTATGAGTCAACCGTTTCGAGTCTCTGATACGCTAAAACACATGAAA
GAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGGAAATTGACGAAACT
CTATGAAGAGTATCAAAGAGGAAACCAATTAGTCAACTTTTAGAGCATATTG
AAAAGTCCCTCTCAAAGGTGAATGCTTAATATTGTTGATGGTAAAGAGA
GATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTATTAGT
AA

SEQ ID NO. 7404

STRAIN H36B

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATACACATT
ACGGGACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAAGAGAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTTACGAAACAATGCTTATGATAAAATCTCTGGTTA
ATTGATTTGTTAAAAGAAGGGAGATCTTAGCCCAAGTATCTGATGCAGG
AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCCGTCTATCTATACCAGGAGCTAGCGCTGGTATTACT
GCTCTCATCGCTTCAGGTTTAGCTCCACAACCTCATATTTTTTATGGCTT
CTTACCGGTAAGCAAGGTCAACAATAACTTTTTTGAACAAGAAAG
ATTACCTGAAACACAATCTTTTATGAGTCAACCGTTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTATGGAGATCGCCAAGTTGTTTTAGT
ACCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAAACCAATTAGTCA
AATCTTTAGGGCATATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTT
ATTGTTGATGGTAAAGAGAGATCTGAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7405

STRAIN 18RS21

GAAATGCAAGTTCAAAAAAGTTTTAAATCAAATATACATT
ACGGAACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATG
ACTTTTCGTGCCATTAGGATTTTAAAGAGAAGTTGATTTTATTTGTGCAGA
GGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTA
AACAAATTAGTTTTTACGAAACAATGCTTACGATAAAATCTCTGGTTA
ATTGATTTGTTAAAAGAAGGGAAATCTTAGCCCAAGTATCTGATGCAGG

Table 74: Comparative Sequences relating to SAG1572

AATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTG
AAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATFACT
GCTCTCATCGCTTCAGGTTTAGCTCCACACCTCATATTTTTTATGGCTT
CTTACCACGTAAGAAAGGTCACAAATAACTTTCTTTGAAACAAAGCAAG
ATTACCCCTGAAACACAAATCTTTATGAGTCACCGTTTCGAGTCTCTGAT
ACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGT
ACGCGAATTGACGAAACTCTATGAAAGATATCAAAGAGGAACCATTAGTC
AACTTTTAGAGCATATGAAAAGGTCCTCTCAAAGGTGAATGCTTAATT
ATTGTTGATGGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACA
AGATCCACTAGTATTAGTAA

SEQ ID NO. 7406

STRAIN M732

GAAATGCAAGTTCAAAAAGTTTTAAATCAAAT
ATACATTACGGAACACTCTATCTAGTCCCACTCCAATTGGTAATCTAGA
TGATATGACTTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTT
GTGCAGAGGATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATT
ACTACTAAAACAAATTAGTTTTTCACGAAACCAATGCTTACGATAAAATCTC
TGGGTTAATTGATTTGTAAAAGAAGGGAATCTTTAGCCCAAGTATCTG
ATGCAAGGAATGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCT
GCTATTGAAGGGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGG
TATTACTGCTCTCATCGCTTCAGGTTTAGCTCCACAACTCATATTTTTT
ATGGCTTCTTACCACGTAAGAAAGGTCACAAATAACTTTCTTTGAAACA
AAGCAAGATTACCCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGT
CTCTGATACGCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTG
TTTTAGTACGCGAATTGACGAACTCTATGAAGAGTATCAAAGAGGAACC
ATTAGTCAACTTTTAGAGCATATTGAAAAGGTCCTCTCAAAGGTGAATG
CTTAATTATGTTGATGGTAAGAGAGATACCGAGCGAGTGAAGACAGTA
GCCAACAGATCCACTAGTATTAGTAA

SEQ ID NO. 7407

STRAIN COHI

GAAATGCAAGTTCAAAAAGTTTTAAATCAAATATACATTAC
GGAACTCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGAC
TTTTCGTGCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGG
ATACACGAAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAA
CAAATTAGTTTTTCACGAAACCAATGCTTACGATAAAATCTCTGGGTTAAT
TGATTTGTTAAAAGAAGGGAATCTTTAGCCCAAGTATCTGATGCAGGAA
TGCCCTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAA
GGGATATCCAGTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCT
TCTCATCGCTTCAGGTTTAGCTCCACAACTCATATTTTTTATGGCTTCT
TACCAGTTAAGAAAGGTCACAAATAACTTTCTTTGAAACAAGCAAGAT
TACCTGAAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATAC
GCTAAAACACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTAC
GCGAATTGACGAAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAA
CTTTTAGAGCATATTGAAAAGGTCCTCTCAAAGGTGAATGCTTAATTAT
TGTTGATGGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAG
ATCCACTAGTATTAGTAA

SEQ ID NO. 7408

STRAIN M781

AAATGCAAGTTCAAAAAGTTTTAAATCAAATATACATTACGGAACACTC
TATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGTGC
CATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACGAA
ATACGGACTTTTACTCAAGCACTTTGATATTACTACTAAAACAAATAGT
TTTTACGAAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTGTT
AAAAGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTA
TTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATC
CCAGTTGATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGC
TTCAGGTTTAGCTCCACAACTCATATTTTTTATGGCTTCTTACCAGTA
AGAAAGGTCACAAATAACTTTCTTTGAAACAAGCAAGATTACCCTGAA
ACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAAACA
CATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATTGA
CGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAGAG
CATATTGAAAAGGTCCTCTCAAAGGTGAATGCTTAATTATTGTTGATGG
TAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAG
TATTAGTAA

A

SEQ ID NO. 7409

STRAIN CJB110

GAAATGCAAGTTCAAAAAGTTTTAAATCAAATACACATTACGGGACAC
TCTATCTAGTCCCACTCCAATTGGTAATCTAGATGATATGACTTTTCGT
GCCATTAGGATTTTAAGAGAAGTTGATTTTATTTGTGCAGAGGATACACG
AAATACGGGACTTTTACTCAAGCACTTTGATATTACTACTAAAACAAATTA
GTTTTACGAAACCAATGCTTACGATAAAATCTCTGGGTTAATTGATTTG
TTAAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTC
TATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGGGA
TCCCGGCTGATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATC
GCTTCAGGTTTAGCTCCACAACTCATATTTTTTATGGCTTCTTACCAGG
TAGAAGAGGTCACAAATAACTTTCTTTGAAACAAGAAAGATTACCCTG
AAACACAAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTAAA
ACATGAAAGAGATTTACGGAGATCGCCAAGTTGTTTTAGTACGCGAATT

Table 74: Comparative Sequences relating to SAG1572

GACGAACTCTATGAAGAGTATCAAAGAGGAACCATTAGTCAACTTTTAG
GGCATATTGAAAAAGTCCCTCTCAAAGGTGAATGCTTAATTATTGTTGAT
GGTAAGAGAGATACCGAGCGAGTGAAGACAGTAGCCAACAGATCCACT
AGTATTAGTAA

SEQ ID NO. 7410

STRAIN 1169NT

TGCAAGTTCAAAAAAGTTTAAATCAAATACACATTATGGGACACTCTAT
CTAGTCCCAACTCCAATTGGTAATCTAGATGATGACTTTTCGTGCCAT
TAGGATTTAAGAGAGAGTTGaTTTTATTGTGTCAGAGGATACACGAAATA
CGGACITTTTACTCAAGCACCTTTGATaTTACTACTAAACAATTAGTtTTT
cACGAACACAATGCTTACGATAAAATCTCTGGGTTAATTGATTtGTTAAA
AGAAGGGAAATCTTTAGCCCAAGTATCTGATGCAGGAATGCCCTCTATTT
CTGACCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGGATATCCCA
GTTGTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTCATCGCTTC
AGGTTTAGCTCCACAACCTCATATTTTTATGGCTTCTTACCACGTAAGA
AAGGTCAACAATAACTTTTTTTGAAACAaAGCAAGATTATCTCTGAAACA
CAAATCTTTTATGAGTCACCGtTTCGAGTCTCTGATACGCTAAAAACACAT
GAAAGAGATTTACGGAGATCGCCAAGTGTTTTAGTACGCGAATTGACgA
AACTCTATGAAGAGTATCAAAGAGGAACCATTaGTCAACTTTTAGAGCAT
ATTGAAAAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGtTGATGGTAA
GAGAGAtaCCGAGCGAGTGAAGACAGTAGCCAACAAGATCCACTAGTAT
TAGTAA

SEQ ID NO. 7411

STRAIN JM9130013

GAAATGCAAGTTCAAAAAAGTTTAAATCAAATACACATTACGGGA
CACTCTATCTAGTCCCAACTCCAATTGGTAATCTAgATGATATGACTTTT
CGTGCCATTAGGATTTTAAGAGAAGTTGATTTTTATTGTGTCAGAGGATAC
ACGAAATACGGGACTTTTACTCAAGCACCTTTGATATTACTACTAAACAAA
TTAGTTTTTACGAACACAATGCTTATGATAAAATCTCTGGGTTAATTGAT
TTGTTAAAGAAGGGAGATCTTTAGCCCAAGTATCTGATGCAGGAATGCC
CTCTATTTCTGACCCAGGACATGACCTTGTCAAGGCTGCTATTGAAGGGG
ATATCCCGGTGCTATCTATACCAGGAGCTAGCGCTGGTATTACTGCTCTC
ATCGCTTCAAGTTTAGCTCCACAACCTCATATTTTTATGGCTTCTTACC
GCCFAAGCAAGTCAACAAATAACtTTTTTTGAAACAaAGAAAGATTACC
CTGAAACACAATCTTTTATGAGTCACCGTTTCGAGTCTCTGATACGCTA
AAACACATGAAGAGATTTATGGAGATCGCCAAGTGTTTTAGTACGCGA
ATTGACGAAACTCTATGAAGAGTATCAAaGAGGAACCATTAGTCAACTTT
TAGGGCATATTGaaaAGGTCCCTCTCAAAGGTGAATGCTTAATTATTGTT
GATGGTAAAGAGATACTGAGCGAGTGAAGACAGTAGCCAACAAGATCC
AGTAGTATTAGTAA

PRETTY of: /biotmp/msa323014.2{*} March 28, 2003 02:40 ..

Table with 5 columns: sequence identifier, alignment offset, and sequence alignment. Includes entries for msa323014.2{343_18RS21} through msa323014.2{343_JM9130013} and a Consensus line.

Table with 5 columns: sequence identifier, alignment offset, and sequence alignment. Includes entries for msa323014.2{343_18RS21} through msa323014.2{343_JM9130013} and a Consensus line.

Table with 5 columns: sequence identifier, alignment offset, and sequence alignment. Includes entries for msa323014.2{343_18RS21} through msa323014.2{343_090} and a Consensus line.

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_CJB110}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
msa323014.2{343_H36B}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
msa323014.2{343_JM9130013}	GTGCCATTAG	GATTTTAAGA	GAAGTTGATT	TTATTTGTGC	AGAGGATACA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	151				200
msa323014.2{343_A909}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_COH1}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M732}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_M781}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_2603}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_1169NT}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_090}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_CJB110}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_H36B}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
msa323014.2{343_JM9130013}	CGAAATACGG	GACTTTTACT	CAAGCCTTT	GATATTACTA	CTAAACAAAT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	201				250
msa323014.2{343_A909}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_COH1}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M732}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_M781}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_2603}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_1169NT}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_090}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_CJB110}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_H36B}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
msa323014.2{343_JM9130013}	TAGTTTTAC	GAACACAATG	CTTAcGATAA	AATCTCTGGG	TTAATTGATT
Consensus	*****	*****	****-*****	*****	*****
msa323014.2{343_18RS21}	251				300
msa323014.2{343_A909}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_COH1}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_M732}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_M781}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_2603}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_1169NT}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_090}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_CJB110}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_H36B}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
msa323014.2{343_JM9130013}	TGTTAAAAGA	AGGGaATCT	TTAGCCCAAG	TATCTGATGC	AGGAATGCC
Consensus	*****	*****-****	*****	*****	*****
msa323014.2{343_18RS21}	301				350
msa323014.2{343_A909}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_COH1}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_M732}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_M781}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_2603}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_1169NT}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_090}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_CJB110}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_H36B}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
msa323014.2{343_JM9130013}	TCTATTTCTG	ACCCAGGACA	TGACCTTGTC	AAGGCTGCTA	TTGAAGGGGg
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	351				400
msa323014.2{343_A909}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_COH1}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M732}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_M781}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_2603}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_1169NT}	tATCCCaGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_090}	gATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_CJB110}	gATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_H36B}	tATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
msa323014.2{343_JM9130013}	tATCCCGt	GTATCTATAC	CAGGAGCTAG	CGCTGGTATT	ACTGCTCTCA
Consensus	-*****-*	*****	*****	*****	*****
msa323014.2{343_18RS21}	401				450
msa323014.2{343_A909}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCc
msa323014.2{343_COH1}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCc
msa323014.2{343_M732}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCc
msa323014.2{343_M781}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCc
msa323014.2{343_2603}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCc
msa323014.2{343_1169NT}	TCGCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCc

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_090}	TCGCCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
msa323014.2{343_CJB110}	TCGCCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
msa323014.2{343_H36B}	TCGCCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
msa323014.2{343_JM9130013}	TCGCCTTCAGG	TTTAGCTCCA	CAACCTCATA	TTTTTTATGG	CTTCTTACCg
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_A909}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_COH1}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_M732}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_M781}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_2603}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_1169NT}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGc	AAGATTAcCC
msa323014.2{343_090}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTAcCC
msa323014.2{343_CJB110}	CGTAAGaAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTAcCC
msa323014.2{343_H36B}	CGTAAGcAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTAcCC
msa323014.2{343_JM9130013}	CGTAAGcAAG	GTCAACAAAT	AACTTTcTTT	GAAACAAAGa	AAGATTAcCC
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_A909}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_COH1}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_M732}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_M781}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_2603}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_1169NT}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_090}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_CJB110}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_H36B}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
msa323014.2{343_JM9130013}	TGAAACACAA	ATCTTTTATG	AGTCACCGTT	TCGAGTCTCT	GATACGCCTAA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_A909}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_COH1}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_M732}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_M781}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_2603}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_1169NT}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_090}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_CJB110}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_H36B}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
msa323014.2{343_JM9130013}	AACACATGAA	AGAGATTATc	GGAGATCGCC	AAGTTGTTTT	AGTACGCGAA
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_A909}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_COH1}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_M732}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_M781}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_2603}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_1169NT}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_090}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_CJB110}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_H36B}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
msa323014.2{343_JM9130013}	TTGACGAAAC	TCTATGAAGA	GTATCAAAGA	GGAACCATTA	GTCACCTTTT
Consensus	*****	*****	*****	*****	*****
msa323014.2{343_18RS21}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_A909}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_COH1}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_M732}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_M781}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_2603}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_1169NT}	AGaGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_090}	AGgGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_CJB110}	AGgGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_H36B}	AGgGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
msa323014.2{343_JM9130013}	AGgGCATATT	GAAAAGTCC	CTCTCAAAGG	TGAATGCTTA	ATTATTGTTG
Consensus	**.....	*****	*****	*****	*****
msa323014.2{343_18RS21}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_A909}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_COH1}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_M732}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_M781}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_2603}	ATGGTAAGAG	AGATACcGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA

Table 74: Comparative Sequences relating to SAG1572

msa323014.2{343_1169NT}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_090}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_CJB110}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_H36B}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
msa323014.2{343_JM9130013}	ATGGTAAGAG	AGATACCGAG	CGAGTGAAAG	ACAGTAGCCA	ACAAGATCCA
Consensus	*****	*****_***	*****	*****	*****
	751				800
msa323014.2{343_18RS21}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_A909}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_COH1}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M732}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_M781}	cTAGTATTAG	TAAA-----	-----	-----	-----
msa323014.2{343_2603}	cTAGTATTAG	TAAAagaata	tatcgctaata	ggtgataaaa	ctaatcaagc
msa323014.2{343_1169NT}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_090}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_CJB110}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_H36B}	cTAGTATTAG	TAA-----	-----	-----	-----
msa323014.2{343_JM9130013}	gTAGTATTAG	TAA-----	-----	-----	-----
Consensus	-*****	*****	*****	*****	*****
	801				850
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	gataaaaaaa	gtagcaaaag	aatttaactct	caatagacaa	gaactctatg
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	851		867		
msa323014.2{343_18RS21}	-----	-----	-----	-----	-----
msa323014.2{343_A909}	-----	-----	-----	-----	-----
msa323014.2{343_COH1}	-----	-----	-----	-----	-----
msa323014.2{343_M732}	-----	-----	-----	-----	-----
msa323014.2{343_M781}	-----	-----	-----	-----	-----
msa323014.2{343_2603}	ctagtttcca	tgattta	-----	-----	-----
msa323014.2{343_1169NT}	-----	-----	-----	-----	-----
msa323014.2{343_090}	-----	-----	-----	-----	-----
msa323014.2{343_CJB110}	-----	-----	-----	-----	-----
msa323014.2{343_H36B}	-----	-----	-----	-----	-----
msa323014.2{343_JM9130013}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 7412

STRAIN 2603 frame: 1

MEMQVQKSFKSNHYGTLVLPVTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
DITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PV
VSI PGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDY PETQI FYESPFRVS
DTLKHMKIY GDRQVVLVRELTKLYEYQRGTISQLLEHIEKVPLKGECL I IVDGKR DTE
RVKSSQQDPLVLV

SEQ ID NO. 7413

STRAIN 090 frame: 1

EMQVQKSFKSNHYGTLVLPVTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGI PVV
SIPGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDY PETQI FYESPFRVSD
TLKHMKIY GDRQVVLVRELTKLYEYQRGTISQLLGHIEKVPLKGECL I IVDGKR DTER
VKDSSQQDPLVLV

SEQ ID NO. 7414

STRAIN A909 frame: 2

VQKSFKSNHYGTLVLPVTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
DITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDY PETQI FYESPFRVSD
TLKHMKIY GDRQVVLVRELTKLYEYQRGTISQLLGHIEKVPLKGECL I IVDGKR DTER
VKDSSQQDPLVLV

SEQ ID NO. 7415

STRAIN H36B frame: 1

EMQVQKSFKSNHYGTLVLPVTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHF
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITALIASGLAPQPHI FYGFLPRKKGQITFFETKQDY PETQI FYESPFRVSD
TLKHMKIY GDRQVVLVRELTKLYEYQRGTISQLLGHIEKVPLKGECL I IVDGKR DTER
VKDSSQQDPLVLV

SEQ ID NO. 7416

Table 74: Comparative Sequences relating to SAG1572

STRAIN 18RS21 frame: 1
EMQVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDRTER
VKDSSQQDPLVLV

SEQ ID NO. 7417
STRAIN M732 frame: 1
EMQVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDRTER
VKDSSQQDPLVLV

SEQ ID NO. 7418
STRAIN COH1 frame: 1
EMQVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDRTER
VKDSSQQDPLVLV

SEQ ID NO. 7419
STRAIN M781 frame: 3
MQVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDI
TTKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVS
IPGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDT
LKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDRTERV
KDSSQQDPLVLV

SEQ ID NO. 7420
STRAIN CJB110 frame: 1
EMQVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGGI PVV
SIPGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDRTER
VKDSSQQDPLVLV

SEQ ID NO. 7421
STRAIN 1169NT frame: 3
QVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFDIT
TKQISFHEHNAYDKISGLIDLKKEGKSLAQVSDAGMPSISDPGHDLVKAIEGDI PVVSI
PGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSDTL
KHMKEIYGDRQVVLVRELTKLYEYQRTISQLLEHIEKVPLKGECLIIVDGKRDRTERVK
DSSQQDPLVLV

SEQ ID NO. 7422
STRAIN JM9130013 frame: 1
EMQVQKSFKSNHYGTYLVLVPTPIGNLDDMTFRAIRILREVDFICAEDTRNTGLLLKHFD
ITTKQISFHEHNAYDKISGLIDLKKEGRSLAQVSDAGMPSISDPGHDLVKAIEGDI PVV
SIPGASAGITAIASGLAPQPHIFYGFLPRKKGQQITFFETKQDYPETQIFYESPFRVSD
TLKHMKEIYGDRQVVLVRELTKLYEYQRTISQLLGHIEKVPLKGECLIIVDGKRDRTER
VKDSSQQDPVVLV

msa324064.2{343_18RS21} -emqVQKSPK SNiHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT 50
msa324064.2{343_A909} ---VQKSPK SNiHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_M781} ---mqVQKSPK SNiHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_2603} memqVQKSPK SNiHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_COH1} -emqVQKSPK SNiHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_M732} -emqVQKSPK SNiHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_1169NT} ---qVQKSPK SNtHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_090} -emqVQKSPK SNtHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_CJB110} -emqVQKSPK SNtHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_H36B} -emqVQKSPK SNtHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
msa324064.2{343_JM9130013} -emqVQKSPK SNtHYGTYLVL VPTPIGNLDD MTFRAIRILR EVDFICAEDT
Consensus *---***** **-***** ***** ***** *****

msa324064.2{343_18RS21} 51 RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP 100
msa324064.2{343_A909} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_M781} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_2603} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_COH1} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_M732} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_1169NT} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_090} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_CJB110} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_H36B} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
msa324064.2{343_JM9130013} RNTGLLLKHFD DITTKQISFH EHNAYDKISG LIDLKKEGKS LAQVSDAGMP
Consensus ***** ***** ***** ***** *****-.. *****

Table 74: Comparative Sequences relating to SAG1572

	101			150
msa324064.2{343_18RS21}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_A909}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_M781}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_2603}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_COH1}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_M732}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_1169NT}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_090}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_CJB110}	SISDPGHDLV	KAAIEGgIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_H36B}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFLP
msa324064.2{343_JM9130013}	SISDPGHDLV	KAAIEGdIPV	VSIPGASAGI	TALIASGLAP QPHIFYGFI.P
Consensus	*****	*****_**	*****	*****
	151			200
msa324064.2{343_18RS21}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_A909}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_M781}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_2603}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_COH1}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_M732}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_1169NT}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_090}	RKkGQQITFF	ETKkDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_CJB110}	RKkGQQITFF	ETKkDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_H36B}	RKkGQQITFF	ETKqDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
msa324064.2{343_JM9130013}	RKkGQQITFF	ETKkDYPETQ	IFYESPPFRVS	DTLKHMKIY GDRQVVLVRE
Consensus	**-*	*****	*****	*****
	201			250
msa324064.2{343_18RS21}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_A909}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_M781}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_2603}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_COH1}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_M732}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_1169NT}	LTKLYEEYQR	GTISQLLeHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_090}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_CJB110}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_H36B}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
msa324064.2{343_JM9130013}	LTKLYEEYQR	GTISQLLgHI	EKVPLKGECL	IIVDGKRDTE RVKDSSQDDP
Consensus	*****	*****_**	*****	*****
	251			289
msa324064.2{343_18RS21}	LVLV-----	-----	-----	-----
msa324064.2{343_A909}	LVLV-----	-----	-----	-----
msa324064.2{343_M781}	LVLV-----	-----	-----	-----
msa324064.2{343_2603}	LVLVkeyian	gdktnqaikk	vakefnlnrq	elyasfhdI
msa324064.2{343_COH1}	LVLV-----	-----	-----	-----
msa324064.2{343_M732}	LVLV-----	-----	-----	-----
msa324064.2{343_1169NT}	LVLV-----	-----	-----	-----
msa324064.2{343_090}	LVLV-----	-----	-----	-----
msa324064.2{343_CJB110}	LVLV-----	-----	-----	-----
msa324064.2{343_H36B}	LVLV-----	-----	-----	-----
msa324064.2{343_JM9130013}	vVLV-----	-----	-----	-----
Consensus	-*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7501
 STRAIN 2603
 ATGAGCGTATATGTTAGTGGAAATAGGAATTATT
 TCTTCTTTGGGAAAGAATTATAGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGA
 ATTTCTAAACATTTATATAAAAAATCAGCACTCTATTTTAGAATCTTATACAGGAAGCATA
 ACTAGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTAAATTTGCT
 TTTACCGCTTTGAGAGGGCTCTTGCTTCTCAGGTGTTAATTTAAAGCTTATCATAT
 ATTGCTGTGTGTTTAGGGACCTCACTTGGGGAAAGAGTGTGGTCAAATGCCTTGAT
 CAATTTGAAGAAGGAGAGCGTCAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTAC
 CATATGCTGATGAATFGATGGCTTATCATGATATTGTTGGAGCTTCGTATGTATTTCA
 ACCGCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACAATFACCTCAAGATGGC
 GATTGTGATTTAGCTATTTGTTGGTGGCTGTGATGAGTTAAGTGATATTTCTTTAGCAGGC
 TTCACATCACTAGGAGCTATAATACAGAAATGGCATGTGAGCCCTATTCTCTGGAAAA
 GGAATCAATTTGGGTGAGGGCGCTGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCT
 AAATATGAAAAATTTACGGTGGTCTTATFACCTCAGATGGTTATCATATAACAGCACCT
 AAGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGTATT
 GACTACAGTGAGATTGACTATATTAACGGTCAAGGTACAGGTAAGTCAAGCTAATGATAAA
 ATGGAAAAAATATGATGTAAGTTTTTCCGACAACGACATTTGATCAGCAGTACCAAG
 GGGCAAACGGGTCATCTCTAGGGCTGCAAGTATTATCGAATGATTAATTTGTTAGCG
 GCAATAGAGGAACAGACTGTACCAGCACTAAAATGAGATTGGGATAGAAGGTTTTCCA
 GAAAAATTTGCTCATCAAAAAGAGAGAATACCCAATAAGAAATGCTTTAAATTTTTCG
 TTTGCTTTTGGTGGAAATAAGTAGTGGTGTCTTATTGTCATCTTTAGATTCACTCTAGAA
 ACATFACCTGCTAGAGAAAAATCTTAAAATGGCTATCTTATCATCTGTGCTTCCATTCT
 AAGAATGAATCACCTTCTATAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAA
 GCATTACGCTTTAAAGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAA
 ATGGATGATTTTTCCAAAATGGTTGCCGTAACACAGCTCAAGCACTAATAGAAAGCAAT
 ATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTTGATTTTACAACACTTTCTGGA
 CCAGTTGAGGTTGTTGAGGTTATTGAAAAGCAAATCAACAAGAGGATATGCACATGTT
 TCTGCTTCCAGATTCCGTTTACGTAATGAATGCAGCAGCTGGTATGCTTTCTATCATT
 TTTAAAAATAACAGGTCCTTTATCTGTCATTTTCGACAAATAGTGGAGCGCTTGATGGTATA
 CAATATGCCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTTCTGTTTCTGCT
 AATCAGTGGACAGACATGAGTTTTTATGTTGGTGGCAACAATTAACCTATGATAGTCAAATG
 TTTGTCGGTCTGATTTATGTTTCAGCACAAAGTCTCTCTCGTCAAGCATTGGATAATCT
 CCTATAATATTAGGTAGTAAACAATTAATAATAGCCATAAAAACATTACAGATGTGATG
 ACTATTTTGTGATCTGCGCTCAAATTTATTATCAGACTTAGGACTAACCCATAAAAGAT
 ATCAAAGGTTTCCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATGATTTCTTA
 GCGAACTGTCTGAGTATTATAATATGCCAAACCTTGCTTCTGGTCAAGTTGGATTTTCA
 TCTAATGTTGCTGGTGAAGAAGTGGACTATAGTTAATGAAAGTATAGAAAAAGGCTAT
 TATTTAGTCTATCTTATTCGATCTTCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7502
 STRAIN 090
 ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGaATTAT
 AGCGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACA
 TTTATATAAAAAATCAGCACTCFATTTTGAATCTTATACAGGAAGCATAA
 CTAGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTT
 AAATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTCAGGTGTTAA
 TTTAAAAGCTTATCATAAATATGCTGTGTGTTTAGGGACCTCACTTGGGG
 GAAAGAGTCTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGT
 CAAGTAGATGCTAGTTTATTAGAAAAAGCATCTGTTTACCATATTGCTGA
 TGAATGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAA
 CCGCTGTTCTGCAAGTAATAATGCCGTAATAATAGGAACACAATTACTT
 CAAGATGGCGAATGTGATTTAGCTATTTGTTGGTGGCTGTGATGAGTTAAG
 TGATATTTCTTTAGCAGGCTTCAATCACTAGGAGCTATTAATACAGAAA
 TGGCATGTGAGCCCTATTTCTCTGGAAAAGGAATCAATTTGGGTGAGGGC
 GCTGTTTTGTTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAA
 AATTATCGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTA
 AGCCAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAA
 GCAGGTATTGACTACAGTGAGATTGACTATATTAACGGTCAAGGTACAGG
 TACTCAAGCTAATGATAAAAAAGAAAAAATATGATGGTAAAGTTTTC
 CGACAACGACATTTGATCAGCAGTACCAAGGGGCAACGGGTCACTACTA
 GGGGCTGCAAGTATATCGAATTTGATTAATTTAGCGGCAATAGAGGA
 ACAGACTGTACCAGCACTAAAATGAGATTGGGATAGAAGGTTTTCCAG
 AAAATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTA
 AATTTTCTGTTGCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCATC
 TTTAGATTCACTCTAGAAACATTACCTGCTAGAGAAAATCTTAAAATGG
 CTATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATA
 ACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTT
 TAAAGGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAA
 TGGATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATA
 GAAAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATTTGT
 ATTTACAACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTATTGAAAAGC
 AAATCACAACAGAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTT
 ACAGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTAAAATAAC
 AGGTCCTTTATCTGCTATTTGACAAATAGTGGAGCGCTTGTGTTATAC
 AATATGCCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTTCT
 GTTTCTGCTAATCAGTGGACAGACATGAGTTTTATGTTGGTGGCAACAAT
 AAACCTATGATAGTCAAATGTTTGTGCGGTTCTGATTTGTTTCAAGCAAG
 TCCTCTCTGCTCAAGCAATGGATAATTTCTCCTATAAATATTAGGTAGTAAA
 CAATTAATAATATAGCCATAAAAACATTACAGATGTGATGACTATTTTTGA
 TGCTGCGCTCAAATTTATTATCAGACTTAGGACTAACCCATAAAAGATA
 TCAAAGGTTTCGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTCAAGATT
 GATTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCTTC

Table 75: Comparative Sequences relating to SAG0671

TGGTCAGTTTGGATTTTCATCTAATGGTGTGGTGAAGAAGCTGGACTATA
CTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATTATTTCG
ATCTTTGGTGGTATCTCTTTTGGCTATTATTGAAAAAAGG

SEQ ID NO. 7503

STRAIN A909

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATT
ATAGCGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAA
CATTATATAAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCAT
AACTAGTGACCCAGAGGTTCTCGAGCAATACAAAGATGAGACACGTAATT
TTAAATTTGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTT
AATTTAAAAGCTTATCATAAATTTGCTGTGTGTTTAGGGACCTCACTTGG
GGGAAAGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGC
GTCAAGTAGATGCTAGTATTATAGAAAAAGCATCTGTTTACCATATGCT
GATGAATTTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTT
AACCCGCTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTAC
TTCAGATAGCGGATTTGTGATTTAGCTATTGTGGTGGCTGTGATGAGTTA
AGTGATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGA
AATGGCATGTGACGCCATTCTTCTGAAAAGGAATCAATTTGGGTGAG
GGCTGGTTTGTGTTCTTGTCAAAGATCAGTCTTAGCTAAATATGGA
AAAATTTACGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACC
TAAGCCAAACAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACT
AAGCAGGTATTGACTACAGTGAATTTGACTATATTAACGGTCAAGGTACA
GGTACTCAAGCTAATGATAAATGAAAAAATATGTATGGTAAAGTTTTT
CCCGACAACGACATTTGATCAGCAGTACCAAGGGGCAAACGGGTCACTC
TAGGGGCTCAGGTTATTATCGAATGATTAAATGTTTTCAGCGCAATAGAG
GAACAGACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCC
AGAAAATTTTGTCTATCATCAAAAGAGAGAAATACCCAATAAGAAATGCTT
TAAATTTTTCGTTTGGCTTTTGGTGAATAATAGTGGTGTCTTATTGTCA
TCTTTAGATTTCACTCTAGAAAACATFACCTGCTAGAGAAAATCTTAAAAAT
GGCTATCTTATCATCTGTGCTTCCATTTCTAAGAATGAATCACTTTCTA
TAACCTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGC
TTTAAAGGGGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAA
AATGGATGATTTTTCAAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAA
TAGAAAGCAATAATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAAT
GTATTTTCAACACTTTCTGACCAGTTGAGGTTGTGAAGGTATTGAAAA
GCAAACTCAACACGAAGGATATGCACATGTTTCTGCTTCAAGCTTCCCGT
TTACAGTAATGAATGCAGCAGCTGGTATGCTTTCTATCAITTTTAAAATA
ACAGTCTCTTATCTGTCTATTTCGACAAATAGTGGAGCGCTTGTATGAT
ACAATATGCCAAGGAAATGATGCGTAAACGATAATCTAGACTATGTGATTC
TTGTTTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACA
TTAACTATGATAGTCAAAATGTTTGTCCGTTCTGATTTATGTTCAAGACA
AGTCTCTCTCTCGTCAAGCATGGATAAATCTCCTATAATATTAGGTAGTA
AACAAATAAAATATAGCCATAAAACATTCACAGATGTGATGACTATTTTT
GATGCTGCGCTTCAAAATTTATTTATCAGACTTAGGACTAACCCATAAAGA
TATCAAAGTTTTCGTTTGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGAT
ATGATTTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCT
TCTGGTCAAGTTTGGATTTTCTATCTAATGGTGTGGTGAAGAAGCTGGACTA
TACTGTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTCTATCTTATT
CGATCTTCGGTGGTATCTCTTTTGGCTATTATTGAAAAAAGG

SEQ ID NO. 7504

STRAIN H36B

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGA
GCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTTAT
ATAAAAATCACGACTCTATTTTAGAATCTTATACAGGAAGCATAAATAGT
GACCCAGAGGTTCTCGAGCAATACAAAGATGAGACACGTAATTTTAAAT
TGCTTTTACCCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTTAA
AAGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAAAG
AGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGT
AGATGCTAGTTTATTTAGAAAAAGCATCTGTTTACCATATTTGCTGATGAAT
TGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCGCC
TGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAAGA
TGGCGATTGTGATTTAGCTATTGTGGTGGCTGTGATGAGTTAAGTGATA
TTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGGCA
TGTACGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCTGG
TTTTGTTGTTCTTGTCAAAGATCAGTCTTAGCTAAATATGAAAAAATTA
TCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCTAAGCCA
ACAGGTGAAGGGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGG
TATTGACTACAGTGAATTTGACTATATTAAAGGTTACCGTACAGGTACTC
AAGCTAATGATAAATGAAAAAATATGTATGGTAAAGTTTTTCCCGACA
ACGACATTTGATCAGCAGTACCAAGGGGCAAACGGGTCACTCTAGGGGC
TGCAGTATTATCGAATTTGATTAATTTGTTTAGCGGCAATAGAGGAACAGA
CTGTACCGCAACTAAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAAAT
TTTTGTTCTATCATCAAAAGAGAGAAATACCCAATAAGAAATGCTTTTAAATTT
TTCGTTTGTCTTTGGTGAATAAATAGTGGTGTCTTATTGTCTATCTTTAG
ATTCACCTTAGAAAAACTTACCTGCTAGAGAAAATCTTAAAAATGGCTATC
TTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTA
TGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCAATTACGCTTTAAAG
GGCTAGACCACCAAACTGTCAACCCAGCACAAATTTAGGAAAATGGAT
GATTTTTTCAAAAATGGTTGCCGTAACCAACAGCTCAAGCACTAATAGAAA
CAATATTAATCTAAAAAACAAGATACTTCAAAAGTAGGAATTTGATTTA
CAACACTTTCTGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAATC

Table 75: Comparative Sequences relating to SAG0671

ACAACAGAAGGATATGCACATGTTTCTGCTTCACGATTCCTGGTTTACAGT
AATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTAAAATAACAGGTC
CTTTATCTGTCAATTTCCGACAAATAGTGGAGCGCTTGATGGTATACAATAT
GCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCCTGTTTC
TGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAACCT
ATGATAGTCAAATGTTTGTGCGTTCTGATFATTGTTTCAGCACAAGTCTCTC
TCTCGTCAAGCATTTGGATAATTTCTCCTATAATATAGGTAGTAAACAATT
AAAATATAGCCATAAAAACATTACAGATGTGATGACTATTTTTGATGCTG
CGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAA
GGTTTCGTTTGAATGAGCGGAAGAGGAGGAGTTAGTTTCAATTTATGATTT
CTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTTGGTC
AGTTTGGATTTTCACTAATGGTGTGGTGAAGAACTGGACTATACTGTT
AATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTTTCCGATCTT
CGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7505

STRAIN 18RS21

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
ATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAAATA
GTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
TTTGTCTTTTACCCTTTTGAAGAGGCTCTTGTCTTCTCAGGTGTTAATTT
AAAAGCTTATCATAATATTTGCTGTGTGTTTAGGGACCTCACITGGGGGA
AGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
ATTGATGGCTTATCATGATATTTGTTGGGAGCTTCGTATGTTATTTCAACCG
CCTGTTTCGCAAGTAATAATGCGTAATAATTAGGAACACAATTTACTTCAA
GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
TATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAAATACAGAAATGG
CATGTCAGCCCTTATTTCTTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
GGTTTTGTTGTTCTTGTCAAAGATCAGTCCCTTAGCTAAATATGGAAAAAT
TATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAGC
CAACAGGTGAAGGGGGCGCACAGATTGCAAAGCAGCTAGTACTCAAGCA
GGTATTGACTACAGTGTGATTTGACTATTTAAACGGTTCACGGTACAGGTAC
TCAAGCTAATGATAAAAATGGAAAAAATAATGATGGTAAGTTTTTCCCGA
CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTTAGGG
GCTGCAGGTATTATCGAATTGATTAATGTTTAGCGGCAATAGAGGAACA
GACTGTACAGCAACTAAAATGAGATTGGGATAGAAGTTTTTCCAGAAA
ATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
TTTTGTTTTGCTTTTGGTGAATAATAGTGGTGTCTTATTGTCTATCTTT
AGATTACCTCTAGAAACATTTACCTGCTAGAGAAAATCTTAAATGGCTA
TCTTATCATCTGTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAACC
TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
AGGGCTAGACCACCCAAAACCTGTCAACCCAGCACAATTTAGGAAAATGG
ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
AGCAATATTAAATCTAAAAAAAACAAGATACTTCAAAGTAGGAATTTGATTT
TACAACAATTTCTGGACAGTTGAGGTTGTTGAAGGTATTGAAAAGCAAA
TCACAACAGAAGGATATGCACATGTTTCTGCTTACGATTTCCGTTTACA
GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGG
TCCTTTATCTGTCAATTTGACAAAATAGTGGAGCGCTTGTATGGTATACAAT
ATGCCAAGGAAAATGATGCGTAACGATAATCTAGACTATGTGATTTCTTGT
TCTGTCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTA
CTATGATAGTCAAATGTTTGTGCGTTCTGATTTATTGTTTCAGCACAAGTCC
TCTCTCGTCAAGCATTGGATAATTTCTCCTATAATATTAGGTAGTAAACAA
TTAAAATATAGCCATAAAAACATTTACAGATGTGATGACTATTTTTGATGC
TGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
AAGGTTTTGTTTGAATGAGCGGAAGAGGAGTTAGTTTCAATTTATGAT
TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTTGG
TCAGTTTGGATTTTCACTAATGGTGTGGTGAAGAACTGGACTATACTG
TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATTTTCCGATCTT
TTCGGTGGTATCTCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7506

STRAIN M732

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
CGAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
TATATAAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAAATA
AGTGACCCAGAGGTTCTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCCTTTTGAAGAGGCTCTTGTCTTCTCAGGTGTTAATTT
TAAAAGCTTATCATAATATTTGCTGTGTGTTTAGGGACCTCACITGGGGGA
AAGAGTGTGGTCAAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTTGTTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATAATTAGGAACACAATTTACTTCA
AGATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
ATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAAATACAGAAATG
GCATGTCAGCCCTTATTTCTTGGAAAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTTGTTGTTCTTGTCAAAGATCAGTCCCTTAGCTAAATATGGAAAAA
TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTTAAG
CCAAACAGGTGAAGGGGGCGCACAGATTGCAAAGCAGCTAGTACTCAAGC
AGGTATTGACTACAGTGTGATTTGACTATTTAAACGGTTCACGGTACAGGTA
CTCAAGCTAATGATAAAAATGGAAAAAATAATGATGGTAAGTTTTTCCCG
ACAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTCTACTCTTAGG

Table 75: Comparative Sequences relating to SAG0671

GGCTGCAGGTATTATCGAATTGATTAATTGTTTAGCGGCAATAGAGGAAC
 AGACTGTACCAGCACTAAAAATGAGATTGGGATAGAAGGTTTCCAGAA
 AATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAA
 TTTTTCGTTTGCCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 TAGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAAATGGCT
 ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTCTATAAC
 CTATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTA
 AAGGGCTAGACCACCCAAAATCTGCAACCAGCACAATTTAGGAAAATG
 GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
 AAGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTAT
 TTACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 ATCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTAC
 AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTAAAATAACAG
 GTCCTTTATCTGTCATTTGACAAAATAGTGGAGCGCTTGATGGTATACAA
 TATGCCAAGGAAATGATGCGTAACGATTAATCTAGACTATGTGATCTTGT
 TTCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAA
 ACTATGATAGTCAAATGTTTGTGCGTTCTGATTAATGTTCAAGCAAGTC
 CTCTCCTGCAAGCATTGGATAAATCTCCTATAATATTAGGTAGTAAACA
 ATTAAAATATAGCCATAAAAACATTCACAGATGTGATGACTATTTTTGATG
 CTGCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATC
 AAAGGTTTCGTTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCCTCTG
 GTCAGTTTGGATTTTCTAATGGTGTGGTGAAGAAGTGGACTATaCT
 GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTATCTTATTCGAT
 CTTCCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7507
 STRAIN COHI

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAAATTTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTCAACCG
 CCTGTTCTGCAAGTAAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAAATATGAAAAAAT
 TATCCGGTGGTCTTATTACTTCAGATGGTTATCATATAACAGCACCCTAAGC
 CAACAGGTGAAGGGCGGCACAGATTGCAAAGCAGCTAGTGACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTACCGTCAAGGTACAGGTAC
 TCAAGCTAATGATAAAAATGAAAAAATATGATGTTAAGTTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACCGGTCATACTCTAGGG
 GCTGCAAGTATTATCGAATTGATTAATTTGTTAGCGGCAATAGAGGAAACA
 GACTGTACCAGCACTAAAATGAGATTGGGATAGAAGTTTTTCCAGAAA
 ATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGCCTTTGGTGGAAATAATAGTGGTGTCTTATTGTCATCTT
 AGATTACCTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAAATGGCTA
 CTATTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGCTAGACCACCCAAAATCTGCAACCAGCACAATTTAGGAAAATGG
 ATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATTT
 TACAACACTTTCTGGACCAGTTGAGGTTGTTGAAGGTATTGAAAAGCAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTAAAATAACAGG
 TCCCTTATCTGTCATTTGACAAAATAGTGGAGCGCTTGATGGTATACAA
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATCTTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTAA
 CTATGATAGTCAAATGTTTGTGCGTTCTGATTATTGTTCAAGCAAGTCC
 TCTCTCGTCAAGCATTGGATAAATCTCCTATAATATTAGGTAGTAAACAA
 TTTAAAATATAGCCATAAAAACATTCACAGATGTGATGACTATTTTTGATG
 TCGCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCGTTTGAAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGCCTCTG
 TCAGTTTGGATTTTCTAATGGTGTGGTGAAGAAGTGGACTATCTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTATCTTATTCGATC
 TCCGGTGGTATCTCTTTGCTATTATTGAAAAAAGG

SEQ ID NO. 7508
 STRAIN M781

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
 ATATAAAATCAGACTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTGAGCAATACAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATTT
 AAAAGCTTATCATAAATTTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAATGCCTTGTATCAATTTGAAGAAGGAGAGCGTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA

Table 75: Comparative Sequences relating to SAG0671

ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGGATTGFGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGG
 CATGTACGCCCTATTCTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
 TATCGGTGGTCTTATTACTTCAAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGGCGCACAGATTGCAAAGCAGCTAGTACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTACTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAATTTAGCGGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGGCTTTGGTGGAAAAATAGTGGTATCTTATTGTCACTTT
 AGATTCACTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAAAATGGCTA
 TCTTATCATCTGTGTCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAATGTCAACCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTACAGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAAATAACAGG
 TCCTTTATCTGTCACTTTCGACAAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTA
 CTATGATAGTCAAATGTTTGTGGTTCTGATTATTGTTTCAACAGTCC
 TCTCTCGTCAAGCATTGGATAAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAAACATTCAAGATGTGATGACTATTTTGTATGC
 TGGCTTCAAATTTATTAATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCTGTTGGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTTCACTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTTCGATC
 TTTGGTGGTATCTTTTGTCTATTATTGAAAAAAGG

SEQ ID NO. 7509

STRAIN CJB110

ATGTTAGTGGAAATAGGAATTAATTTCTTCTTTGGGAAAGAATTATAGC
 GAGCATAAACAGCATCTCTTCGACTTAAAAGAAGGAATTTCTAAACATTT
 ATATAAAAATCAGCAGCTCTATTTTAGAATCTTATACAGGAAGCATAACTA
 GTGACCCAGAGGTTCTCTGAGCAATACAAAGATGAGACACGTAATTTTAAA
 TTTGCTTTTACCGCTTTTGAAGAGGCTCTTGTCTTCTCAGGTGTTAATTT
 AAAAGCTTATCATAAATTGCTGTGTGTTTAGGGACCTCACTTGGGGGAA
 AGAGTGTGGTCAAATGCTTGTATCAATTTGAAGAAGGAGAGCGCTCAA
 GTAGATGCTAGTTTATTAGAAAAGCATCTGTTTACCATATTGCTGATGA
 ATTGATGGCTTATCATGATATTGTGGGAGCTTCGTATGTTAATTTCAACCG
 CCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCAA
 GATGGCGATTGTGATTAGCTATTTGTGGTGGCTGTGATGAGTTAAGTGA
 TATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAAATACAGAAATGG
 CATGTACGCCCTATTCTCTGGAAAAGGAATCAATTTGGGTGAGGGCGCT
 GGTTTTGTGTTCTTGTCAAAGATCAGTCCTTAGCTAAATATGGAAAAAT
 TATCGGTGGTCTTATTACTTCAAGATGGTTATCATATAACAGCACCTAAGC
 CAACAGGTGAAGGGGGCGCACAGATTGCAAAGCAGCTAGTACTCAAGCA
 GGTATTGACTACAGTGAGATTGACTATATTAATGGTCACGGTACAGGTAC
 TCAAGCTAATGATAAAATGGAAAAAATATGTATGGTAAGTTTTCCCGA
 CAACGACATTGATCAGCAGTACCAAGGGGCAACGGGTACTACTCTAGGG
 GCTGCAGGTATTATCGAATTGATTAATTTAGCGGCAATAGAGGAACA
 GACTGTACAGCAACTAAAAATGAGATTGGGATAGAAGTTTTCCAGAAA
 ATTTTGTCTATCATCAAAGAGAGAATACCCAATAAGAAATGCTTTAAAT
 TTTTCGTTTGGCTTTGGTGGAAAAATAGTGGTATCTTATTGTCACTTT
 AGATTCACTCTAGAAAACATTACCTGCTAGAGAAAATCTTAAAAATGGCTA
 TCTTATCATCTGTGTCTTCCATTTCTAAGAATGAATCACTTTCTATAACC
 TATGAAAAAGTTGCTAGTAATTTCAACGACTTTGAAGCATTACGCTTTAA
 AGGGGCTAGACCACCCAAAATGTCAACCAGCACAAATTTAGGAAAATGG
 ATGATTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGAA
 AGCAATATTAATCTAAAAAACAAGATACTTCAAAGTAGGAATGTATT
 TACAACACTTTCTGGACCAGTTGAGGTTGTGAAGGTATTGAAAAGCAAA
 TCACAACAGAAGGATATGCACATGTTTCTGCTTACAGATTCCCGTTTACA
 GTAATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTAAAAATAACAGG
 TCCTTTATCTGTCACTTTCGACAAAATAGTGGAGCGCTTGATGGTATACAAT
 ATGCCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTGTGT
 TCTGCTAATCAGTGGACAGACATGAGTTTTATGTGGTGGCAACAATTA
 CTATGATAGTCAAATGTTTGTGGTTCTGATTATTGTTTCAAGCACAGTCC
 TCTCTCGTCAAGCATTGGATAAATCTCCTATAATATTAGGTAGTAAACAA
 TTAATAATATAGCCATAAAAACATTCAAGATGTGATGACTATTTTGTATGC
 TGGCTTCAAATTTATTAATCAGACTTAGGACTAACCATAAAAGATATCA
 AAGGTTTCTGTTGGAATGAGCGGAAGAAGGCAGTTAGTTTCAAGTTATGAT
 TTCTTAGCGAACTTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGG
 TCAGTTTGGATTTTCACTAATGGTGTGGTGAAGAACTGGACTATACTG
 TTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTTCGATC
 TTTGGTGGTATCTTTTGTCTATTATTGAAAAAAGG

Table 75: Comparative Sequences relating to SAG0671

SEQ ID NO. 7510

STRAIN 1169NT

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
CGAGCATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATT
TATATAAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACT
AGTGACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAA
ATTTGCTTTTACCGCTTTTGAAGAGGCTCTTGCTTCTTCAGGTGTTAATT
TAAAGCTTATCATAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGGA
AAGAGTGTGGTCAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCA
AGTAGATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATG
AATTGATGGCTTATCATGATATTGTTGGGAGCTTCGTATGTTATTTCAACC
GCCTGTTCTGCAAGTAATAATGCCGTAATATTAGGAACACAATTACTTCA
AGATGGCGATTGTGATTTAGCTATTGTTGGTGGCTGTGATGAGTTAAGTG
ATATTTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATG
GCATGTGAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGC
TGGTTTGTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAAA
TTATCGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAG
CCAACAGGTGAAGGGGGCGCACAGATTGCAAAGCAGCTAGTGACTCAAGC
AGGTATTGACTACAGTGAGATTGACTATATAACGGTCAACGGTACAGGTA
CTCAAGCTAATGATAAAAATGGAAAAAATATGATGGTAAGTTTTCCCGG
ACAAACGACATTGATCAGCAGTACCAGGGGCAACCGGTCATACTTAGG
GGCTGCAGGTATTATCGAATTGATTAATTTGTTTAGCGCAATAGAGGAAC
AGACTGTACCAGCACTAAAATGAGATTGGGATAGAAGGTTTTCCAGAA
AATTTTGTCTATCATCAAAGAGAGAATACCCATAAGAAATGCTTTAAA
TTTTTCTGTTGCTTTTGGTGGAAATAATAGTGGTATCTTATTGTCACTTT
TAGATTCCCTCTAGAAAACATFACCTGCTAGAGAAAATCTTAAAATGGCT
ATCTTATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAAC
CTATGAAAAGTTGCTAGTAAATTTCAACGACTTTGAAGCATTACGCTTTA
AAGGGCTTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATG
GATGATTTTTCCAAAATGGTTGCCGTAACAACAGCTCAAGCACTAATAGA
AAGCAATATTAATCTAAAAAACAAGATCTTCAAAGTAGGAATTTGTAT
TTACAACACTTTCTGGACAGTTGAGGTTGTTGAAGGTTATTGAAAAGCAA
ATCAACAAGAGGATATGCACATGTTTCTGCTTCAGGATTTCCCGTTTAC
AGTAATGAATGCAGCAGCTGGTATGCTTCTATCATTTTTAAAATAACAG
GTCTTTTATCTGTCAITTCGACAAAATAGTGGAGCGCTTGATGGTATACAA
TATGCCAAGGAAATGATGCGTAACAGATAATCTAGACTATGTGATTCTTGT
TTCTGCTAATCAGTGGACAGACATGAGTTTATGTGGTGGCAACAATTA
ACTATGATAGTCAAATGTTTGTGGTCTGATTTATGTTTCAACAGCTC
CTCTCTCGTCAAGCATGGATAATTTCTCTATAATATTAGGTAGTAAACA
ATTTAAAATATAGCCATAAAAACATTCACAGATGTGATGACTATTTTTGATG
CTGGCTTCAAATTTATATCAGACTTAGGACTAACCATAAAAGATATC
AAAGTTTCTGTTTGGAAATGAGCGGAAGAAGGCAGTTAGTTTCAAGATTATG
TTTTCTTAGCGAATGTTCTGAGTATTATAATATGCCAACCTTGCTCTG
GTCAGTTTGGATTTTCTATTAATGGTGGTGGTGAAGAATGGACTATACT
GTTAATGAAAGTATAGAAAAGGGCTATTATTAGTCTTATCTTATTCGAT
CTTTGGTGGTATCTCTTTTGGCTATTATTGAAAAAAGG

SEQ ID NO. 7511

STRAIN JM9130013

ATGTTAGTGGAAATAGGAATTATTTCTTCTTTGGGAAAGAATTATAGCGAG
CATAAACAGCATCTCTTCGACTTAAAGAAGGAATTTCTAAACATTTATA
TAAAATCAGGACTCTATTTTGAATCTTATACAGGAAGCATAACTAGTG
ACCCAGAGGTTCTTGAGCAATACAAAGATGAGACACGTAATTTTAAATTT
GCTTTTACCGCTTTTGAAGAGGCTCTTGGCTTCTTCAGGTGTTAATTTAAA
AGCTTATCATAAATATTGCTGTGTGTTTAGGGACCTCACTTGGGGAAAGA
GTGCTGGTCAAATGCTTGTATCAATTTGAAGAAGGAGAGCGTCAAGTA
GATGCTAGTTTATAGAAAAAGCATCTGTTTACCATATTGCTGATGAATT
GATGGCTTATCATGATAATTGTTGGGAGCTTCGTATGTTATTTCAACCGCTT
GTTCTGCAAGTATAATGCCGTAATATTAGGAACACAATTACTTCAAGAT
GGCGATTGTGATTAGCTATTTGTTGGTGGCTGTGATGAGTTAAGTGATAT
TTCTTTAGCAGGCTTACATCACTAGGAGCTATTAATACAGAAATGGCAT
GTCAGCCCTATTCTTCTGAAAAGGAATCAATTTGGGTGAGGGCGCTGGT
TTTGTGTTCTTGTCAAAGATCAGTCCCTAGCTAAATATGGAAAAAATTAT
CGGTGGTCTTATTACTTTCAGATGGTTATCATATAACAGCACCTAAGCCA
CAGGTGAAGGGGGCGCACAGATTGCAAAGCAGCTAGTGACTCAAGCAGGT
ATTGACTACAGTGAGATTGACTATATAATAACGGTCAACGGTACAGGTA
AGCTAATGATAAAAATGGAAAAAATATGATGGTAAAGTTTTTCCCGACAA
CGACATTGATCAGCAGTACCAGGGGCAACCGGTCATACTTAGGGGCT
GCAGGTATTATCGAATTGATTAATTTGTTAGCGGCAATAGAGGAACAGAC
TGTACAGCAACTAAAATGAGATTGGGATAGAAGGTTTTCCAGAAAATTT
TTGCTATCATCAAAGAGAGAATACCCATAAGAAATGCTTTAAAATTTT
TCGTTTGGCTTTTGGTGGAAATAATAGTGGTGTCTTATTGTTCATCTTTAGA
TTCACCTTAGAAAACATTTACCTGCTAGAGAAAATCTTAAAATGGCTATCT
TATCATCTGTTGCTTCCATTTCTAAGAATGAATCACTTTCTATAACCTAT
GAAAAAGTTGCTAGTAAATTTCAACGACTTTGAAGCATTACGCTTTAAGG
GGCTAGACCACCCAAAACCTGTCAACCCAGCACAAATTTAGGAAAATGGATG
ATTTTTCAAATGGTTGCCGTAACAACAGCTCAAGCCTAATAGAAAAGC
AATATTAAATCTAAAAAACAAGATACTTCAAAGTAGGAATTTGATTTAC
AACACTTTCTGGACCAAGTTGAGGTTGTTGAAGGTTATTGAAAAGCAAAATCA
CAACAGAGGATATGCACATGTTTCTGCTTCAAGATTCCCGTTTACAGTA
ATGAATGCAGCAGCTGGTATGCTTTCTATCATTTTTAAAATAACAGGTC
TTTATCTGTCAATTTGACAAAATAGTGGAGCGCTTGTGATGATACAAATATG

Table 75: Comparative Sequences relating to SAG0671

CCAAGGAAATGATGCGTAACGATAATCTAGACTATGTGATTCTTGTTCCT
GCTAATCAGTGGACAGACATGAGTTTATGTTGGTGGCAACAATAAACA
TGATAGTCAAATCTTTGTCGGTTCGATTATTGTTTCAGCACAAAGTCCTCT
CTCGTCAAGCATGGATAAATCTCCATAATATAGGTAGTAAACAATTA
AAATATAGCCATAAAACATTACAGATGTGATGACTATTTTGTGCTGC
GCTTCAAATTTATTATCAGACTTAGGACTAACCATAAAAGATATCAAAG
GTTTCGTTTGGAAATGAGCGGAAGAGGCAGTTAGTTTCAGATTATGATTTC
TTAGCGAAGCTGTCTGAGTATTATAATATGCCAAACCTTGTCTCTGGTCA
GTTTGGATTTCATCTAATGGTGTCTGGTGAAGAAGTGGACTATACTGTTA
ATGAAAGTATAGAAAAGGGCTATTATTAGTCCATATCTTATTGATCTTC
GGTGTATCTCTTTGCTATTATTGAAAAAAGG

PRETTY of: /biotmp/msa118688.2{*} April 9, 2003 02:55 ..

msa118688.2{361_18RS21} 1 50
msa118688.2{361_A909}
msa118688.2{361_COH1}
msa118688.2{361_H36B}
msa118688.2{361_JM9130013}
msa118688.2{361_M732}
msa118688.2{GBS361_2603} atgagcgtat
msa118688.2{361_090}
msa118688.2{361_1169NT}
msa118688.2{361_CJB110}
msa118688.2{361_M781}
Consensus *****

msa118688.2{361_18RS21} 51 100
msa118688.2{361_A909}
msa118688.2{361_COH1}
msa118688.2{361_H36B}
msa118688.2{361_JM9130013}
msa118688.2{361_M732}
msa118688.2{GBS361_2603}
msa118688.2{361_090}
msa118688.2{361_1169NT}
msa118688.2{361_CJB110}
msa118688.2{361_M781}
Consensus *****

msa118688.2{361_18RS21} 101 150
msa118688.2{361_A909}
msa118688.2{361_COH1}
msa118688.2{361_H36B}
msa118688.2{361_JM9130013}
msa118688.2{361_M732}
msa118688.2{GBS361_2603}
msa118688.2{361_090}
msa118688.2{361_1169NT}
msa118688.2{361_CJB110}
msa118688.2{361_M781}
Consensus *****

msa118688.2{361_18RS21} 151 200
msa118688.2{361_A909}
msa118688.2{361_COH1}
msa118688.2{361_H36B}
msa118688.2{361_JM9130013}
msa118688.2{361_M732}
msa118688.2{GBS361_2603}
msa118688.2{361_090}
msa118688.2{361_1169NT}
msa118688.2{361_CJB110}
msa118688.2{361_M781}
Consensus *****

msa118688.2{361_18RS21} 201 250
msa118688.2{361_A909}
msa118688.2{361_COH1}
msa118688.2{361_H36B}
msa118688.2{361_JM9130013}
msa118688.2{361_M732}
msa118688.2{GBS361_2603}
msa118688.2{361_090}
msa118688.2{361_1169NT}
msa118688.2{361_CJB110}
msa118688.2{361_M781}
Consensus *****

Table 75: Comparative Sequences relating to SAG0671

	251				300
msa118688.2{361_18RS21}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_A909}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_COH1}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_H36B}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_JM9130013}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_M732}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{GBS361_2603}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_090}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_1169NT}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_CJB110}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
msa118688.2{361_M781}	TTAATTTAAA	AGCTTATCAT	AATATTGCTG	TGTGTTTAGG	GACCTCACTT
Consensus	*****	*****	*****	*****	*****
	301				350
msa118688.2{361_18RS21}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_A909}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_COH1}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_H36B}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_JM9130013}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_M732}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{GBS361_2603}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_090}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_1169NT}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_CJB110}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
msa118688.2{361_M781}	GGGGGAAAGA	GTGCTGGTCA	AAATGCCTTG	TATCAATTTG	AAGAAGGAGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa118688.2{361_18RS21}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_A909}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_COH1}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_H36B}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_JM9130013}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_M732}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{GBS361_2603}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_090}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_1169NT}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_CJB110}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
msa118688.2{361_M781}	GCGTCAAGTA	GATGCTAGTT	TATTAGAAAA	AGCATCTGTT	TACCATATTG
Consensus	*****	*****	*****	*****	*****
	401				450
msa118688.2{361_18RS21}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_A909}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_COH1}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_H36B}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_JM9130013}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_M732}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{GBS361_2603}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_090}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_1169NT}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_CJB110}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
msa118688.2{361_M781}	CTGATGAATT	GATGGCTTAT	CATGATATTG	TGGGAGCTTC	GTATGTTATT
Consensus	*****	*****	*****	*****	*****
	451				500
msa118688.2{361_18RS21}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_A909}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_COH1}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_H36B}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_JM9130013}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_M732}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{GBS361_2603}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_090}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_1169NT}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_CJB110}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
msa118688.2{361_M781}	TCAACCGCCT	GTTCTGCAAG	TAATAATGCC	GTAATATTAG	GAACACAATT
Consensus	*****	*****	*****	*****	*****
	501				550
msa118688.2{361_18RS21}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_A909}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_COH1}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_H36B}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_JM9130013}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_M732}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{GBS361_2603}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_090}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_1169NT}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_CJB110}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT
msa118688.2{361_M781}	ACTTCAAGAT	GCGGATTGTG	ATTTAGCTAT	TTGTGGTGGC	TGTGATGAGT

Table 75: Comparative Sequences relating to SAG0671

Consensus	*****	*****	*****	*****	*****
	551				600
msa118688.2{361_18RS21}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_A909}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_COH1}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_H36B}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_JM9130013}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M732}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{GBS361_2603}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_090}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_1169NT}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_CJB110}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
msa118688.2{361_M781}	TAAGTGATAT	TTCTTTAGCA	GGCTTCACAT	CACTAGGAGC	TATTAATACA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118688.2{361_18RS21}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_A909}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_COH1}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_H36B}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_JM9130013}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M732}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{GBS361_2603}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_090}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_1169NT}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_CJB110}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
msa118688.2{361_M781}	GAAATGGCAT	GTCAGCCCTA	TTCTTCTGGA	AAAGGAATCA	ATTTGGGTGA
Consensus	*****	*****	*****	*****	*****
	651				700
msa118688.2{361_18RS21}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_A909}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_COH1}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_H36B}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_JM9130013}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M732}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{GBS361_2603}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_090}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_1169NT}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_CJB110}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
msa118688.2{361_M781}	GGGCGCTGGT	TTTGTGTGTC	TTGTCAAAGA	TCAGTCCTTA	GCTAAATATG
Consensus	*****	*****	*****	*****	*****
	701				750
msa118688.2{361_18RS21}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_A909}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_COH1}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_H36B}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_JM9130013}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M732}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{GBS361_2603}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_090}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_1169NT}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_CJB110}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
msa118688.2{361_M781}	GAAAAATTAT	CGGTGGTCTT	ATTACTTCAG	ATGGTTATCA	TATAACAGCA
Consensus	*****	*****	*****	*****	*****
	751				800
msa118688.2{361_18RS21}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_A909}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_COH1}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_H36B}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_JM9130013}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M732}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{GBS361_2603}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_090}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_1169NT}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_CJB110}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
msa118688.2{361_M781}	CCTAAGCCAA	CAGGTGAAGG	GGCGGCACAG	ATTGCAAAGC	AGCTAGTGAC
Consensus	*****	*****	*****	*****	*****
	801				850
msa118688.2{361_18RS21}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_A909}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_COH1}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_H36B}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_JM9130013}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_M732}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{GBS361_2603}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_090}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_1169NT}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA
msa118688.2{361_CJB110}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAC	GGTCACGGTA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_M781}	TCAAGCAGGT	ATTGACTACA	GTGAGATTGA	CTATATTAAT	GGTCACGGTA
Consensus	*****	*****	*****	*****	*****
	851				900
msa118688.2{361_18RS21}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_A909}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_COH1}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_H36B}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_JM9130013}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M732}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{GBS361_2603}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_090}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_1169NT}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_CJB110}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
msa118688.2{361_M781}	CAGGTACTCA	AGCTAATGAT	AAAATGGAAA	AAAATATGTA	TGGTAAGTTT
Consensus	*****	*****	*****	*****	*****
	901				950
msa118688.2{361_18RS21}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_A909}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_COH1}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_H36B}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_JM9130013}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M732}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{GBS361_2603}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_090}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_1169NT}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_CJB110}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
msa118688.2{361_M781}	TTCCCGACAA	CGACATTGAT	CAGCAGTACC	AAGGGGCAAA	CGGGTCATAC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa118688.2{361_18RS21}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_A909}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_COH1}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_H36B}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_JM9130013}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M732}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{GBS361_2603}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_090}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_1169NT}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_CJB110}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
msa118688.2{361_M781}	TCTAGGGGCT	GCAGGTATTA	TCTGAATTGAT	TAATTGTTTA	GCGGCAATAG
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa118688.2{361_18RS21}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_A909}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_COH1}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_H36B}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_JM9130013}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M732}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{GBS361_2603}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_090}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_1169NT}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_CJB110}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
msa118688.2{361_M781}	AGGAACAGAC	TGTACCAGCA	ACTAAAAATG	AGATTGGGAT	AGAAGGTTTT
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa118688.2{361_18RS21}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_A909}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_COH1}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_H36B}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_JM9130013}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M732}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{GBS361_2603}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_090}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_1169NT}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_CJB110}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
msa118688.2{361_M781}	CCAGAAAATT	TTGTCTATCA	TCAAAGAGAGA	GAATACCCAA	TAAGAAATGC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa118688.2{361_18RS21}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_A909}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_COH1}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_H36B}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_JM9130013}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_M732}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{GBS361_2603}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_090}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_1169NT}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	GTCTTATTGT
Consensus	*****	*****	*****	*****	*****

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_CJB110}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT
msa118688.2{361_M781}	TTTAAATTTT	TCGTTTGCTT	TTGGTGGAAA	TAATAGTGGT	aTCTTATTGT
Consensus	*****	*****	*****	*****	*****
1151					
msa118688.2{361_18RS21}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_A909}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_COH1}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_H36B}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_JM9130013}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_M732}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{GBS361_2603}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_090}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_1169NT}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_CJB110}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
msa118688.2{361_M781}	CATCTTTAGA	TTCACCTCTA	GAAACATTAC	CTGCTAGAGA	AAATCTTAAA
Consensus	*****	*****	*****	*****	*****
1201					
msa118688.2{361_18RS21}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_A909}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_COH1}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_H36B}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_JM9130013}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_M732}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{GBS361_2603}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_090}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_1169NT}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_CJB110}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
msa118688.2{361_M781}	ATGGCTATCT	TATCATCTGT	TGCTTCCATT	TCTAAGAATG	AATCACTTTC
Consensus	*****	*****	*****	*****	*****
1251					
msa118688.2{361_18RS21}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_A909}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_COH1}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_H36B}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_JM9130013}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_M732}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{GBS361_2603}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_090}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_1169NT}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_CJB110}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
msa118688.2{361_M781}	TATAACCTAT	GAAAAAGTTG	CTAGTAATTT	CAACGACTTT	GAAGCATTAC
Consensus	*****	*****	*****	*****	*****
1301					
msa118688.2{361_18RS21}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_A909}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_COH1}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_H36B}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_JM9130013}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_M732}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{GBS361_2603}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_090}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_1169NT}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_CJB110}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
msa118688.2{361_M781}	GCTTTAAAGG	GGCTAGACCA	CCCAAACTG	TCAACCCAGC	ACAATTTAGG
Consensus	*****	*****	*****	*****	*****
1351					
msa118688.2{361_18RS21}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_A909}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_COH1}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_H36B}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_JM9130013}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_M732}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{GBS361_2603}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_090}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_1169NT}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_CJB110}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
msa118688.2{361_M781}	AAAATGGATG	ATTTTTCCAA	AATGGTTGCC	GTAACAACAG	CTCAAGCACT
Consensus	*****	*****	*****	*****	*****
1401					
msa118688.2{361_18RS21}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_A909}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_COH1}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_H36B}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_JM9130013}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_M732}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{GBS361_2603}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_090}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_1169NT}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_CJB110}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
msa118688.2{361_M781}	AATAGAAAGC	AATATTAATC	TAAAAAACA	AGATACTTCA	AAAGTAGGAA
	Consensus	*****	*****	*****	*****
	1451				1500
msa118688.2{361_18RS21}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_A909}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_COH1}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_H36B}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_JM9130013}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_M732}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{GBS361_2603}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_090}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_1169NT}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_CJB110}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
msa118688.2{361_M781}	TTGTATTAC	AACACTTTCT	GGACCAGTTG	AGGTTGTTGA	AGGTATTGAA
	Consensus	*****	*****	*****	*****
	1501				1550
msa118688.2{361_18RS21}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_A909}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_COH1}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_H36B}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_JM9130013}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_M732}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{GBS361_2603}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_090}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_1169NT}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_CJB110}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
msa118688.2{361_M781}	AAGCAAATCA	CAACAGAAGG	ATATGCACAT	GTTTCTGCTT	CACGATTCCC
	Consensus	*****	*****	*****	*****
	1551				1600
msa118688.2{361_18RS21}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_A909}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_COH1}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_H36B}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_JM9130013}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_M732}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{GBS361_2603}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_090}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_1169NT}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_CJB110}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
msa118688.2{361_M781}	GTTTACAGTA	ATGAATGCAG	CAGCTGGTAT	GCTTCTATC	ATTTTAAAA
	Consensus	*****	*****	*****	*****
	1601				1650
msa118688.2{361_18RS21}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_A909}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_COH1}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_H36B}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_JM9130013}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_M732}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{GBS361_2603}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_090}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_1169NT}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_CJB110}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
msa118688.2{361_M781}	TAACAGGTCC	TTTATCTGTC	ATTTTCGACAA	ATAGTGGAGC	GCTTGATGGT
	Consensus	*****	*****	*****	*****
	1651				1700
msa118688.2{361_18RS21}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_A909}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_COH1}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_H36B}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_JM9130013}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_M732}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{GBS361_2603}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_090}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_1169NT}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_CJB110}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
msa118688.2{361_M781}	ATACAATATG	CCAAGGAAAT	GATGCGTAAC	GATAATCTAG	ACTATGTGAT
	Consensus	*****	*****	*****	*****
	1701				1750
msa118688.2{361_18RS21}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_A909}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_COH1}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_H36B}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_JM9130013}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_M732}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{GBS361_2603}	TCTTGTCTTCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{361_090}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_1169NT}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_CJB110}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
msa118688.2{361_M781}	TCTTGTTCCT	GCTAATCAGT	GGACAGACAT	GAGTTTTATG	TGGTGGCAAC
Consensus	*****	*****	*****	*****	*****
1751					
msa118688.2{361_18RS21}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_A909}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_COH1}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_H36B}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_JM9130013}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_M732}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{GBS361_2603}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_090}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_1169NT}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_CJB110}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
msa118688.2{361_M781}	AATTAACCTA	TGATAGTCAA	ATGTTTGTTCG	GTTCTGATTA	TTGTTCCAGCA
Consensus	*****	*****	*****	*****	*****
1801					
msa118688.2{361_18RS21}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_A909}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_COH1}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_H36B}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_JM9130013}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M732}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{GBS361_2603}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_090}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_1169NT}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_CJB110}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
msa118688.2{361_M781}	CAAGTCCTCT	CTCGTCAAGC	ATTGGATAAT	TCTCCTATAA	TATTAGGTAG
Consensus	*****	*****	*****	*****	*****
1851					
msa118688.2{361_18RS21}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_A909}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_COH1}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_H36B}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_JM9130013}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M732}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{GBS361_2603}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_090}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_1169NT}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_CJB110}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
msa118688.2{361_M781}	TAAACAATTA	AAATATAGCC	ATAAAACATT	CACAGATGTG	ATGACTATTT
Consensus	*****	*****	*****	*****	*****
1901					
msa118688.2{361_18RS21}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_A909}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_COH1}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_H36B}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_JM9130013}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_M732}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{GBS361_2603}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_090}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_1169NT}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_CJB110}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
msa118688.2{361_M781}	TTGATGCTGC	GCTTCAAAT	TTATTATCAG	ACTTAGGACT	AACCATAAAA
Consensus	*****	*****	*****	*****	*****
1951					
msa118688.2{361_18RS21}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_A909}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_COH1}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_H36B}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_JM9130013}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M732}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{GBS361_2603}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_090}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_1169NT}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_CJB110}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
msa118688.2{361_M781}	GATATCAAAG	GTTTCGTTTG	GAATGAGCGG	AAGAAGGCAG	TTAGTTCAGA
Consensus	*****	*****	*****	*****	*****
2001					
msa118688.2{361_18RS21}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_A909}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_COH1}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_H36B}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_JM9130013}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M732}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
2050					
msa118688.2{361_18RS21}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_A909}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_COH1}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_H36B}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_JM9130013}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M732}	TTATGATTTT	TTAGCGAACT	TGTCTGAGTA	TTATAATATG	CCAAACCTTG

Table 75: Comparative Sequences relating to SAG0671

msa118688.2{GBS361_2603}	TTATGATTC	TTAGCGAACT	TGCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_090}	TTATGATTC	TTAGCGAACT	TGCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_1169NT}	TTATGATTC	TTAGCGAACT	TGCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_CJB110}	TTATGATTC	TTAGCGAACT	TGCTGAGTA	TTATAATATG	CCAAACCTTG
msa118688.2{361_M781}	TTATGATTC	TTAGCGAACT	TGCTGAGTA	TTATAATATG	CCAAACCTTG
Consensus	*****	*****	*****	*****	*****
	2051				2100
msa118688.2{361_18RS21}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_A909}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_COH1}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_H36B}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_JM9130013}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_M732}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{GBS361_2603}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_090}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_1169NT}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_CJB110}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
msa118688.2{361_M781}	CTTCTGGTCA	GTTTGGATT	TCATCTAATG	GTGCTGGTGA	AGAAGCTGGAC
Consensus	*****	*****	*****	*****	*****
	2101				2150
msa118688.2{361_18RS21}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_A909}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_COH1}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_H36B}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_JM9130013}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M732}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{GBS361_2603}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_090}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_1169NT}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_CJB110}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
msa118688.2{361_M781}	TATACTGTTA	ATGAAAGTAT	AGAAAAGGGC	TATTATTTAG	TCCTATCTTA
Consensus	*****	*****	*****	*****	*****
	2151				2193
msa118688.2{361_18RS21}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_A909}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_COH1}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_H36B}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_JM9130013}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M732}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{GBS361_2603}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_090}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_1169NT}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_CJB110}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
msa118688.2{361_M781}	TTCGATCTTc	GGTGGTATCT	CTTTTGCTAT	TATTGAAAAA	AGG
Consensus	*****	*****	*****	*****	***

SEQ ID NO. 7512

STRAIN 2603 frame: 1

MSVYVSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDS ILESYTGSI TSDPEVPEQ
YKDETRNPKFAFAFEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQV
DASLLEKASVYHI ADEL MAYHDI VGASYVI STACSASNNAV ILGTQLLQDGDCLAI CGG
CDELSDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGI IGGI
ITSDGYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDY INGHGTGTQANDKMEKNMYGKF
FPTTLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQKR
EYPIRNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKAILSSVASI SKNESLSITY
EKVASNFNDFEALRFK GARPPKTVNPAQFRKMDDFS KMVAVTTAQALIESNINLKKQDTS
KVGIVFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS IIFKITGPLSV
ISTNSGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSA
QVLSRQALDNP IILGSKQLKYSHKTFDVTMI FDAALQNLSDLG LTI KD I KGFVWNER
KAVSSDYDFLANLSEYNNMPLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYSI F
GGISFAIEKR

SEQ ID NO. 7513

STRAIN 090 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDS ILESYTGSI TSDPEVPEQYKDE
TRNPKFAFAFEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQV DASEL
LEKASVYHI ADEL MAYHDI VGASYVI STACSASNNAV ILGTQLLQDGDCLAI CGG CDE
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYKGI IGGI LITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDY INGHGTGTQANDKMEKNMYGKF FPT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQKREYPI
RNALNFSFAFGGNNSGVLLSSLDSPLETL PARENLMKAILSSVASI SKNESLSITYE KVA
SNFNDFEALRFK GARPPKTVNPAQFRKMDDFS KMVAVTTAQALIESNINLKKQDTSKVG
VFTTSLGPPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS IIFKITGPLSVI STN
SGALDGIQYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYSQMFVGS DYCSA QVLS
RQALDNP SPIILGSKQLKYSHKTFDVTMI FDAALQNLSDLG LTI KD I KGFVWNERKAV
SSDYDFLANLSEYNNMPLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVSYSI FGGIS
FAIEKR

SEQ ID NO. 7514

STRAIN A909 frame: 3

Table 75: Comparative Sequences relating to SAG0671

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES...
TRNFKFAFTA...
LEKASVYHIADELMAYHDI...
SDISLAGFTSLGA...
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPPTT...
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI...
RNALNFSFAFGGNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA...
SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMAVAVTTAQUALIESNINLKKQDTSKVGI...
VFTTLLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS I I FKI TGPLSVI STN...
SGALDGI QYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS...
RQALDNSPI I LGSKQLKYSHKTFDVTM I FDAALQNL LSDLGLTI KD I KGFVWNERKKA V...
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS...
FAIIEKR

SEQ ID NO. 7515

STRAIN H36B frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES...
TRNFKFAFTA...
LEKASVYHIADELMAYHDI...
SDISLAGFTSLGA...
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPPTT...
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI...
RNALNFSFAFGGNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA...
SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMAVAVTTAQUALIESNINLKKQDTSKVGI...
VFTTLLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS I I FKI TGPLSVI STN...
SGALDGI QYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS...
RQALDNSPI I LGSKQLKYSHKTFDVTM I FDAALQNL LSDLGLTI KD I KGFVWNERKKA V...
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS...
FAIIEKR

SEQ ID NO. 7516

STRAIN 18RS21 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES...
TRNFKFAFTA...
LEKASVYHIADELMAYHDI...
SDISLAGFTSLGA...
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPPTT...
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI...
RNALNFSFAFGGNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA...
SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMAVAVTTAQUALIESNINLKKQDTSKVGI...
VFTTLLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS I I FKI TGPLSVI STN...
SGALDGI QYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS...
RQALDNSPI I LGSKQLKYSHKTFDVTM I FDAALQNL LSDLGLTI KD I KGFVWNERKKA V...
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS...
FAIIEKR

SEQ ID NO. 7517

STRAIN M732 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES...
TRNFKFAFTA...
LEKASVYHIADELMAYHDI...
SDISLAGFTSLGA...
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPPTT...
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI...
RNALNFSFAFGGNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA...
SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMAVAVTTAQUALIESNINLKKQDTSKVGI...
VFTTLLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS I I FKI TGPLSVI STN...
SGALDGI QYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS...
RQALDNSPI I LGSKQLKYSHKTFDVTM I FDAALQNL LSDLGLTI KD I KGFVWNERKKA V...
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS...
FAIIEKR

SEQ ID NO. 7518

STRAIN COH1 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES...
TRNFKFAFTA...
LEKASVYHIADELMAYHDI...
SDISLAGFTSLGA...
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPPTT...
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI...
RNALNFSFAFGGNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA...
SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMAVAVTTAQUALIESNINLKKQDTSKVGI...
VFTTLLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS I I FKI TGPLSVI STN...
SGALDGI QYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS...
RQALDNSPI I LGSKQLKYSHKTFDVTM I FDAALQNL LSDLGLTI KD I KGFVWNERKKA V...
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS...
FAIIEKR

SEQ ID NO. 7519

STRAIN M781 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES...
TRNFKFAFTA...
LEKASVYHIADELMAYHDI...
SDISLAGFTSLGA...
GYHITAPKPTGEGAAQIAKQLVTQAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPPTT...
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQTVPATKNEIGIEGFPENFVYHQKREYPI...
RNALNFSFAFGGNSGVLLSSLDSPLETL PARENLMKMAILSSVASISKNESLSITYEKVA...
SNFNDFEALRFKRGARPPKTVNPAQFRKMDDFSKMAVAVTTAQUALIESNINLKKQDTSKVGI...
VFTTLLSGPVEVVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLS I I FKI TGPLSVI STN...
SGALDGI QYAKEMMRNDNLDYVILV SANQWTDMSFMWWQQLNYDSQMFVGS DYCSAQVLS...
RQALDNSPI I LGSKQLKYSHKTFDVTM I FDAALQNL LSDLGLTI KD I KGFVWNERKKA V...
SSDYDFLANLSEYYNMPNLASGQFGFSSNGAGEELDYTVNESIEKGYLVLVLSYSIFGGIS...
FAIIEKR

Table 75: Comparative Sequences relating to SAG0671

LEKASVYHIADELMAYHDI VGASYVISTACASANNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSTIYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQUALIESNINLKKQDTSKVGI
VFTTSLGPEVEVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFDVMTI FDAALQNLSDLGTLTKDIKGFVWNERKKA
SSDYDFLANLSEYNNMPLASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7520

STRAIN CJB110 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
TRNPKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSTIYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQUALIESNINLKKQDTSKVGI
VFTTSLGPEVEVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFDVMTI FDAALQNLSDLGTLTKDIKGFVWNERKKA
SSDYDFLANLSEYNNMPLASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7521

STRAIN 1169NT frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
TRNPKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSTIYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQUALIESNINLKKQDTSKVGI
VFTTSLGPEVEVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFDVMTI FDAALQNLSDLGTLTKDIKGFVWNERKKA
SSDYDFLANLSEYNNMPLASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
FAIEKR

SEQ ID NO. 7522

STRAIN JM9130013 frame: 3

VSGIGI ISSLGKNYSEHKQHLFDLKEGISKHLYKNHDSILES YTGSI TSDPEVPEQYKDE
TRNPKFAFTAFEEALASSGVNLKAYHNI AVCLGTS LGGKSAGQNALYQFEEGERQVDASL
LEKASVYHIADELMAYHDI VGASYVISTACASANNAVILGTQLLDGDCDLAICGGCDEL
SDISLAGFTSLGAINTEMACQPYSSGKGINLGEAGFVVLVKDQSLAKYGKI IGGITSD
GYHITAPKPTGEGAAQIAKQLVTOAGIDYSEIDYINGHGTGTQANDKMEKNMYGKFFPTT
TLISSTKGQTGHTLGAAGI IELINCLAAIEEQVTPATKNEIGIEGFPENFVYHQREYPI
RNALNFSFAFGGNSGILLSSLDSPLETLPAENLKMALSSVASISKNESLSTIYEKVA
SNFNDFEALRFKGARPPKTVNPAQFRKMDDFSKMVAVTTAQUALIESNINLKKQDTSKVGI
VFTTSLGPEVEVEGIEKQITTEGYAHVSASRFPFTVMNAAAGMLSIFKITGPLSVISTN
SGALDGIQYAKEMMRNDNLDYVILVSNQWTDMSFMWWQQLNYDSQMFVGSYCSAQVLS
RQALDNSPI ILGSKQLKYSHKTFDVMTI FDAALQNLSDLGTLTKDIKGFVWNERKKA
SSDYDFLANLSEYNNMPLASGQFGFSSNGAGEELDYTVNESIEKGYLVLSYSIFGGIS
FAIEKR

PRETTY of: /biotmp/ma118713.2{*} April 9, 2003 02:54 ..

Table with 5 columns: sequence identifier, position 1, position 50, position 51, position 100. Rows include various strain identifiers like msa118713.2{361_090} and a consensus row.

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_A909}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_COH1}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_H36B}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_JM9130013}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{361_M732}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
msa118713.2{GBS361_2603}	ITSDPEVPEQ	YKDETRNFKF	AFTAFEEALA	SSGVNLKAYH	NIAVCLGTSL
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_1169NT}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_CJB110}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M781}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_18RS21}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_A909}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_COH1}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_H36B}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_JM9130013}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{361_M732}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
msa118713.2{GBS361_2603}	GGKSAGQNAL	YQFEEGERQV	DASLLEKASV	YHIADELMAY	HDIVGASYVI
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_1169NT}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_CJB110}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_M781}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_18RS21}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_A909}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_COH1}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_H36B}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_JM9130013}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{361_M732}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
msa118713.2{GBS361_2603}	STACSASNNA	VILGTQLLQD	GDCDLAICGG	CDELSDISLA	GFTSLGAIN
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_1169NT}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_CJB110}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M781}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_18RS21}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_A909}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_COH1}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_H36B}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_JM9130013}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{361_M732}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
msa118713.2{GBS361_2603}	EMACQPYSSG	KGINLGEAG	FVVLVKDQSL	AKYGKIIGGL	ITSDGYHITA
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_1169NT}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_CJB110}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M781}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_18RS21}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_A909}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_COH1}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_H36B}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_JM9130013}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{361_M732}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
msa118713.2{GBS361_2603}	PKPTGEGAAQ	IAKQLVTQAG	IDYSEIDYIN	GHGTGTQAND	KMEKNMYGKF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_1169NT}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_CJB110}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M781}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_18RS21}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_A909}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_COH1}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_H36B}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_JM9130013}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{361_M732}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
msa118713.2{GBS361_2603}	FPTTLLISST	KGQTGHTLGA	AGIIELINCL	AAIEBQTVPA	TKNEIGIEGF
Consensus	*****	*****	*****	*****	*****
msa118713.2{361_090}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_1169NT}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_CJB110}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK
msa118713.2{361_M781}	PENFVYHQKR	EYPIRNALNF	SFAPGGNSG	ILLSSLDSP	ETLPARENLK

Table 75: Comparative Sequences relating to SAG0671

msa118713.2{361_18RS21}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_A909}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_COH1}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_H36B}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_JM9130013}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{361_M732}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
msa118713.2{GBS361_2603}	PENFVYHQKR	EYPIRNALNF	SFAFGGNSG	VLLSSLDSPL	ETLPARENLK
Consensus	*****	*****	*****	*****	*****
	401				450
msa118713.2{361_090}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_1169NT}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_CJB110}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_M781}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_18RS21}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_A909}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_COH1}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_H36B}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_JM9130013}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{361_M732}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
msa118713.2{GBS361_2603}	MAILSSVASI	SKNESLSITY	EKVASNFNDF	EALRFKQAR	PKTVPNAQFR
Consensus	*****	*****	*****	*****	*****
	451				500
msa118713.2{361_090}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_1169NT}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_CJB110}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M781}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_18RS21}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_A909}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_COH1}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_H36B}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_JM9130013}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{361_M732}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
msa118713.2{GBS361_2603}	KMDDFSKMVA	VTTAQALIES	NINLKKQDTS	KVGIVFTTLS	GPVEVVEGIE
Consensus	*****	*****	*****	*****	*****
	501				550
msa118713.2{361_090}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_1169NT}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_CJB110}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M781}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_18RS21}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_A909}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_COH1}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_H36B}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_JM9130013}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{361_M732}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
msa118713.2{GBS361_2603}	KQITTEGYAH	VSASRFPFTV	MNAAAGMLSI	IFKITGPLSV	ISTNSGALDG
Consensus	*****	*****	*****	*****	*****
	551				600
msa118713.2{361_090}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_1169NT}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_CJB110}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_M781}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_18RS21}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_A909}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_COH1}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_H36B}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_JM9130013}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{361_M732}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
msa118713.2{GBS361_2603}	IQYAKEMMRN	DNLDYVILVS	ANQWTDMSFM	WWQQLNYDSQ	MFVGSQDYCSA
Consensus	*****	*****	*****	*****	*****
	601				650
msa118713.2{361_090}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_1169NT}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_CJB110}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_M781}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_18RS21}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_A909}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_COH1}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_H36B}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_JM9130013}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{361_M732}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
msa118713.2{GBS361_2603}	QVLSRQALDN	SPIILGSKQL	KYSHKFTFDV	MTIFDAALQN	LLSDLGLTIK
Consensus	*****	*****	*****	*****	*****
	651				700
msa118713.2{361_090}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_1169NT}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD
msa118713.2{361_CJB110}	DIKGFVWNER	KKAVSSDYDF	LANLSEYNYM	PNLASGQFGF	SSNGAGEELD

Table 76: Comparative Sequences relating to SAG0260

SEQ ID NO. 7601

STRAIN 2603

ATGAAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCAGAAAACCGTTTAA
AATAATATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTCTGGA
GCAGGGAAATCTACCTTGATTAATACTATGCTTGGCATGGAAAAAGCAGATAAGGGGAACA
GCTCTTGTTCCTTGATACTCAAATGCCAGATCGTAATATTTTAAATCAAATGGCTATATG
GCTCAATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTTCTTTGGA
AAAATGAAAGGTATTCAAAAAAAGTGAATTAATAACAGCAGATAAATCATATTTCTAAAAGTA
GTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAAAAGA
CGGCTTCTCTAGCCATCGCCCTACTTTGAAAACCCACAGTTTAAATCCTAGATGAACCT
ACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAG
GATGAAGACATTTCTATCTTTATTACAACCCAGTTATGGATGAAGCAGAATTAACAAGT
AAGGTTGCACTACTATTACGTGGAAACATTTATGCTTTGATACTCCATTACATTTAAAA
AAACATTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7602

STRAIN 090

ATTTAAAAAACTACAAAAAGCATATGCCTCAGAAAAGTGTTTTAAATAAT
ATTAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCTC
TGGAGCAGGGAAATCTACCTTGATTAATACTATGCTTGGCATGGAAAAAG
CAGATAAGGGGAACAGCTCTTGTTCCTTGATACTCAAATGCCAGATCGTAAT
ATTTTAAATCAAATGGCTATATGGCTCAATCTGATGCCTTATACGAATC
TTTAACTGCCTTAGAAAATTATTATTCTTTGGAAAAATGAAAGGTATTCT
AAAAAACTGAAATTAATAACAGCAGATAAATCATATTTCTAAAAGTAGTAGAT
CTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGAA
AAGACGGCTTCTCTAGCCATCGCCCTACTTTGAAAACCCACAGTTTAA
TCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAATC
TGGCAAGAGCTAATTAATATTAAGGATGAAGGACGTTCTATCTTTATTAC
AACCCACTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTAT
TACGTGGAACATTTATGCTTTGATACTCCATTACATTTAAAAAAACAA
TTTTAATGTGAGTACTATTGAGGAAGTTTTCTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7603

STRAIN A909

AAAAAAGTCATCGATTAAAAAACTACAAAAAGCATATGCCTCA
GAAACCGTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAATAAT
TGGATTAAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTAATACTA
TGCTTGGCATGGAAAAAGCAGATAAGGGGAACAGCTCTTGTTCCTTGATACT
CAAATGCCAGATCATAATATTTTAAATCAAATGGCTATATGGCTCAATC
TGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCTTTG
GAAAAATGAAAGGTATTCAAAAAAAGTGAATTAATAACAGCAGATAAATCAT
ATTTCTAAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTACTTG
GAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCAGTTATGGATGAAGCAGAATTAACAA
GTAAGGTTGCACTACTATTACGTGGAAACATTTATGCTTTGATACTCCA
TTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7604

STRAIN H36B

AAAAAAGTCATTGATTAAAAAACTACAAAAAGCATATGCC
TCAGAAACCGTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
AATTTGGATTAAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTAATA
CTATGCTTGGCATGGAAAAAGCAGATAAGGGGAACAGCTCTTGTTCCTTGAT
ACTCAAATGCCAGATCGTAATATTTTAAATCAAATGGCTATATGGCTCA
ATCTGATGCCTTATACGAGTCTTTAACTGGCTTAGAAAAATTTATTATTCT
TTGAAAAATGAAAGGTATTCAAAAAAAGTGAATTAATAACAGCAGATAAAT
CATATTTCTAAAAGTAGTAGATCTAGAAAACCAACTTGATAAATTTGTCTC
AGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTCTAGCCATCGCCCTAC
TTGAAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
CCATCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
AGGACGTTCTATCTTTATTACAACCCAGTTATGGATGAAGCAGAATTA
CAAGTAAGGTTGCACTACTATTACGTGGAAACATTTATGCTTTGATACT
CCATTACATTTAAAAAAACAAATTTAATGTGAGTACTATTGAGGAAGTTTT
CTTAAAAGCTGAAGGAGAA

SEQ ID NO. 7605

STRAIN 18RS21

GATTTAAAAAACTACAAAAAGCATATGCCTCAGAAAACCGTTTAAATAA
TATTAAATTTGGAGGTGTTTAAAGGCGAAATAATTGGATTAAATAGGACCCCT
CTGGAGCAGGGAAATCTACCTTGATTAATACTATGCTTGGCATGGAAAAA
GCAGATAAGGGGAACAGCTCTTGTTCCTTGATACTCAAATGCCAGATCGTAA
TATTTTAAATCAAATGGCTATATGGCTCAATCTGATGCCTTATACGAGT
CTTTAACTGGCTTAGAAAAATTTATTATTCTTTGAAAAATGAAAGGTATT
CAAAAAAAGTGAATTAATAACAGCAGATAAATCATATTTCTAAAAGTAGTAGA
TCTAGAAAACCAACTTGATAAATTTGTCTCAGGTTACTCAGGAGGTATGA
AAGACGGCTTCTCTAGCCATCGCCCTACTTTGAAAACCCACAGTTTAA
ATCCTAGATGAACCTACCGTTGGAATTGATCCATCCTTGAGGAGAAAAAT
CTGGCAAGAGCTAATTAATATTAAGGATGAAGGACATTTCTATCTTTATTA
CAACCCAGTTATGGATGAAGCAGAATTAACAAGTAAGGTTGCACTACTA

Table 76: Comparative Sequences relating to SAG0260

TTACGTGGAACATTTATTGCCTTTGATACTCCATTACATTTAAAAACA
ATTTAATGTGAGTACTATTGAGGAAGTTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7606

STRAIN M732

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATACGCCCTCA
GAAACTGTTTAAATAATTAATTTGGAGGTGTTTAAAGGAGAAATAAT
TGGATTAATAGGACCCTCTGGAGCAGGAAATCTACCTTGATTAACACTA
TGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACT
CAAATGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGCTCAATC
TGATGCCCTTACACGAGTCTTAACTGGCTTAGAAAAATTTATTATTCTTTG
GAAAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAACTCAT
ATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAAATTTGTCTCAGG
TTACTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCCTACTTG
GAAACCCACAGTTTAACTCTAGATGAACCTACCGTTGGAATTGATCCA
TCCTTGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAAGGATGAAGG
ACGTTCTATCTTTATTACAACCCAGTTTATGGATGAAGCAGAAATTAACA
GTAAGGTTGCACTACTATTACGTGGAACATTTATTGCCTTTGATACTCCA
TTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTCTT
AAAAGCTGAAGGAGAA

SEQ ID NO. 7607

STRAIN COHI

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATACGCCCTCAGAA
ACTGTTTAAATAATTAATTTGGAGGTGTTTAAAGGAGAAATAATTTGG
ATTAATAGGACCCTCTGGAGCAGGAAATCTACCTTGATTAACACTATGC
TTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTGATACTCAA
ATGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGCTCAATCTGA
TGCTTACACGAGTCTTAACTGGCTTAGAAAAATTTATTATTCTTTGAA
AAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAACTCATATT
TCTAAAGTAGTAGATCTAGAAAACCACTTGATAAAATTTGTCTCAGGTTA
CTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCCTACTTGGAA
ACCCACAGTTTAACTCTAGATGAACCTACCGTTGGAATTGATCCATCC
TTGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAAGGATGAAGGACG
TTCTATCTTTATTACAACCCAGTTTATGGATGAAGCAGAAATTAACAAGTA
AGGTTGCACTACTATTACGTGGAACATTTATTGCCTTTGATACTCCATTA
CAITTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAG

SEQ ID NO. 7608

STRAIN M781

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTAAATAATTAATTTGGAGGTGTTTAAAGGAGA
AATAATGGATTAAATAGGACCCTCTGGAGCAGGAAATCTACCTTGATTA
AAACTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTT
GATACTCAAATGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTTACACGAGTCTTAACTGGCTTAGAAAAATTTATTAT
TCTTTGAAAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATA
ACTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCC
TACTTGGAAACCCACAGTTTAACTCTAGATGAACCTACCGTTGGAAT
GATCCATCCTTGGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCAGTTTATGGATGAAGCAGAA
TAAACAAGTAAGGTTGCACTACTATTACGTGGAACATTTATTGCCTTTGAT
ACTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7609

STRAIN CJB110

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATATG
CCTCAGAAACTGTTTAAATAATTAATTTGGAGGTGTTTAAAGGCGAA
ATAATGGATTAAATAGGACCCTCTGGAGCAGGAAATCTACCTTGATTA
AACTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTTG
ATACTCAAATGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGCT
CAATCTGATGCCCTTATACGAATCTTAACTGCTTAGAAAAATTTATTATT
CTTTGAAAAATGAAAGGTATTCAAAAACTGAATTAACACAGCAGATAA
CTCATATTTCTAAAGTAGTAGATCTAGAAAACCACTTGATAAAATTTGTC
TCAGGTTACTCAGGAGGTATGAAAAGACGGCTTTCTTAGCCATCGCCCT
ACTTGGAAACCCACAGTTTAACTCTAGATGAACCTACCGTTGGAATG
ATCCATCCTTGGAGGAGAAAAATCTGGCAAGAGCTAATTAATTAAGGAT
GAAGGACGTTCTATCTTTATTACAACCCAGTTTATGGATGAAGCAGAA
AACAAGTAAGGTTGCACTACTATTACGTGGAACATTTATTGCCTTTGATA
CTCCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGT
TTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7610

STRAIN 1169NT

AAAAAAGTCATCGATTTAAAAAACTACAAAAAGCATAC
GCCTCAGAAACTGTTTAAATAATTAATTTGGAGGTGTTTAAAGGCGA
AATAATGGATTAAATAGGACCCTCTGGAGCAGGAAATCTACCTTGATTA
AAACTATGCTTGGCATGAAAAAGCAGATAAGGGAACAGCTCTTGTCTT
GATACTCAAATGCCAGATCGTAATATTTAAATCAAATTGGCTATATGGC
TCAATCTGATGCCCTTATACGAATCTTAACTGCTTAGAAAAATTTATTAT

Table 76: Comparative Sequences relating to SAG0260

TCTTTGGAAAAATGAAAAGGTATTCAAAAACTGAATTAACAGCAGATA
ACTCATATTTCTAAAGTAGTAGACTAGAAAACCACTTGATAAAATTTGT
CTCAGGTTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCC
TACTTGGAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATT
GATCCATCCTTGAGGAGAAAATCTGGCAAGAGCTAATTAATATTAAGGA
TGAAGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAAT
TAACAAGTAAGGTTGCACTACTATTACGTTGAAACATATTGCTTTGAT
ACTCCATTACATTTAAAAAAACAATTAATGTGAGTACTATTGAGGAAGT
TTTCTTAAAGCTGAAGGAGAA

SEQ ID NO. 7611

STRAIN JM9130013

AAAAAAGTCATCGATTTAAAAAACTACAAAAGCATATGCC
TCAGAAACCGTTTAAATAATATTAATTTGGAGGTGTTTAAAGGCGAAAT
AATTTGGATTAATAGGACCCCTCTGGAGCAGGGAAATCTACCTTGATTAATA
CTATGCTTTGGCATGGAAAAGCAGATAAGGGAAACAGCTCTTGTTCCTTGT
ACTCAAATGCCAGATCGTAATATTTTAAATCAAATTTGGCTATATGGCTCA
ATCTGATGCCTTATACAGTCTTTAACTGGCTTAGAAAATTTATTATTCT
TTGAAAAAATGAAAGGTATTCAAAAACTGAATTAACAGCAGATAACT
CATATTTCTAAAGTAGTAGACTAGAAAACCACTTGATAAAATTTGTCTC
AGGTTACTCAGGAGGTATGAAAAGACGGCTTCTCTAGCCATCGCCCTAC
TTGAAAACCCACAGTTTAAATCCTAGATGAACCTACCGTTGGAATTGAT
CCATCCTTTGAGGAGAAAATCTGGCAAGAGCTAATTAATATTAAGGATGA
AGGACGTTCTATCTTTATTACAACCCACGTTATGGATGAAGCAGAATTA
CAAGTAAGGTTGCACTACTATTACGTTGAAACATATTGCTTTGATACT
CCATTACATTTAAAAAAACAATTTAATGTGAGTACTATTGAGGAAGTTTT
CTTAAAGCTGAAGGAGAA

PRETTY of: /biotmp/msa134270.2{*} April 10, 2003 02:14 ..

msa134270.2{391_COH1} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AcGCCTCAGA
msa134270.2{391_M732} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AcGCCTCAGA
msa134270.2{391_M781} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AcGCCTCAGA
msa134270.2{391_090} -----ATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
msa134270.2{391_CJB110} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
msa134270.2{391_1169NT} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AcGCCTCAGA
msa134270.2{391_18RS21} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
msa134270.2{391_2603} atgaaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
msa134270.2{391_A909} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
msa134270.2{391_JM9130013} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
msa134270.2{391_H36B} ---aaaaaag tcatcgATTT AAAAAAACTA CAAAAGCAT AtGCCTCAGA
Consensus ***-----*****

msa134270.2{391_COH1} AACtGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGa GAAATAATTG
msa134270.2{391_M732} AACtGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGa GAAATAATTG
msa134270.2{391_M781} AACtGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGa GAAATAATTG
msa134270.2{391_090} AACtGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_CJB110} AACtGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_1169NT} AACtGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_18RS21} AACcGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_2603} AACcGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_A909} AACcGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_JM9130013} AACcGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
msa134270.2{391_H36B} AACcGTTTAA AATAATATTA ATTTGGAGGT GTTTAAAGGc GAAATAATTG
Consensus ***-*****

msa134270.2{391_COH1} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_M732} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_M781} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_090} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_CJB110} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_1169NT} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_18RS21} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_2603} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_A909} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_JM9130013} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
msa134270.2{391_H36B} GATTAATAGG ACCCTCTGGA GCAGGGAAAT CTACCTTGAT TAAAACATG
Consensus *****

msa134270.2{391_COH1} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_M732} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_M781} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_090} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_CJB110} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_1169NT} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_18RS21} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_2603} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA
msa134270.2{391_A909} CTTGGCATGG AAAAAGCAGA TAAGGGAACA GCTCTTGTTT TTGATACTCA

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_JM9130013}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
msa134270.2{391_H36B}	CTTGGCATGG	AAAAAGCAGA	TAAGGGAACA	GCTCTTGTTT	TTGATACTCA
Consensus	*****	*****	*****	*****	*****
	201				250
msa134270.2{391_COH1}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M732}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_M781}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_090}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_CJB110}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_1169NT}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_18RS21}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_2603}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_A909}	AATGCCAGAT	CaTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_JM9130013}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
msa134270.2{391_H36B}	AATGCCAGAT	CgTAATATTT	TAAATCAAAT	TGGCTATATG	GCTCAATCTG
Consensus	*****	*-*****	*****	*****	*****
	251				300
msa134270.2{391_COH1}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M732}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_M781}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_090}	ATGCCCTTAcA	CGAaTCITTA	ACTGcCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_CJB110}	ATGCCCTTAcA	CGAaTCITTA	ACTGcCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_1169NT}	ATGCCCTTAcA	CGAaTCITTA	ACTGcCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_18RS21}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_2603}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_A909}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_JM9130013}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
msa134270.2{391_H36B}	ATGCCCTTAcA	CGAgTCITTA	ACTGgCTTAG	AAAATTTATT	ATTCTTTGGA
Consensus	*****-*	***-*****	****-*****	*****	*****
	301				350
msa134270.2{391_COH1}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_M732}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_M781}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_090}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_CJB110}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_1169NT}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_18RS21}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_2603}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_A909}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_JM9130013}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
msa134270.2{391_H36B}	AAAATGAAAG	GTATTCAAAA	AAC TGAATTA	AAACAGCAGA	TAAC TCATAT
Consensus	*****	*****	*****	*****	*****
	351				400
msa134270.2{391_COH1}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M732}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_M781}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_090}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_CJB110}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_1169NT}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_18RS21}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_2603}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_A909}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_JM9130013}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
msa134270.2{391_H36B}	TTCTAAAGTA	GTAGATCTAG	AAAACCAACT	TGATAAATTT	GTCTCAGGTT
Consensus	*****	*****	*****	*****	*****
	401				450
msa134270.2{391_COH1}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M732}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_M781}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_090}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_CJB110}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_1169NT}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_18RS21}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_2603}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_A909}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_JM9130013}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
msa134270.2{391_H36B}	ACTCAGGAGG	TATGAAAAGA	CGGCTTTCTC	TAGCCATCGC	CCTACTTGGA
Consensus	*****	*****	*****	*****	*****
	451				500
msa134270.2{391_COH1}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M732}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_M781}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_090}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_CJB110}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_1169NT}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_18RS21}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_2603}	AACCCACAG	TTTTAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC

Table 76: Comparative Sequences relating to SAG0260

msa134270.2{391_A909}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_JM9130013}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
msa134270.2{391_H36B}	AACCCACAG	TTTAAATCCT	AGATGAACCT	ACCGTTGGAA	TTGATCCATC
Consensus	*****	*****	*****	*****	*****
	501				550
msa134270.2{391_COH1}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M732}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_M781}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_090}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_CJB110}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_1169NT}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_18RS21}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_2603}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_A909}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_JM9130013}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
msa134270.2{391_H36B}	CTTGAGGAGA	AAAATCTGGC	AAGAGCTAAT	TAATATTAAG	GATGAAGGAC
Consensus	*****	*****	*****	*****	*****
	551				600
msa134270.2{391_COH1}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M732}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_M781}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_090}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_CJB110}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_1169NT}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_18RS21}	aTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_2603}	aTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_A909}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_JM9130013}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
msa134270.2{391_H36B}	gTTCTATCTT	TATTACAACC	CACGTTATGG	ATGAAGCAGA	ATTAACAAGT
Consensus	-*****	*****	*****	*****	*****
	601				650
msa134270.2{391_COH1}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M732}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_M781}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_090}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_CJB110}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_1169NT}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_18RS21}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_2603}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_A909}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_JM9130013}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
msa134270.2{391_H36B}	AAGGTTGCAC	TACTATTACG	TGGAACATT	ATTGCCTTTG	ATACTCCATT
Consensus	*****	*****	*****	*****	*****
	651				700
msa134270.2{391_COH1}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	G-----
msa134270.2{391_M732}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_M781}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_090}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_CJB110}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_1169NT}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_18RS21}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_2603}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_A909}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_JM9130013}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
msa134270.2{391_H36B}	ACATTTAAAA	AAACAATTTA	ATGTGAGTAC	TATTGAGGAA	GTTTTCTTAA
Consensus	*****	*****	*****	*****	*****
	701		714		
msa134270.2{391_COH1}	-----	-----			
msa134270.2{391_M732}	AAGCTGAAGG	AGAA			
msa134270.2{391_M781}	AAGCTGAAGG	AGAA			
msa134270.2{391_090}	AAGCTGAAGG	AGAA			
msa134270.2{391_CJB110}	AAGCTGAAGG	AGAA			
msa134270.2{391_1169NT}	AAGCTGAAGG	AGAA			
msa134270.2{391_18RS21}	AAGCTGAAGG	AGAA			
msa134270.2{391_2603}	AAGCTGAAGG	AGAA			
msa134270.2{391_A909}	AAGCTGAAGG	AGAA			
msa134270.2{391_JM9130013}	AAGCTGAAGG	AGAA			
msa134270.2{391_H36B}	AAGCTGAAGG	AGAA			
Consensus	*****	****			

SEQ ID NO. 7612

STRAIN 2603 frame: 1

KKVIDLKKLQKAYASETVLNNINLEVPFKGEIIGLIGPSGAGKSTLIKTMGMKADKGTALVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQOITHISKVV
DLENQLDKFVSGYSGGMRRLSLAIALLNPTVLIILDEPTVGDIPSLRRKIWQELINIKD
EGHSIFITTHVMDAELTSKVALLLRGNIAFDTPLHLKQKQFNV

SEQ ID NO. 7613

Table 76: Comparative Sequences relating to SAG0260

STRAIN 090 frame: 3
LKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGTALVLD
QMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQOITHISKVVDLENQ
LDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKDEGRSI
FITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7614
STRAIN A909 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7615
STRAIN H36B frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7616
STRAIN 18RS21 frame: 1
DLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGTALVLD
TQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQOITHISKVVDLEN
QLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKDEGHS
IFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7617
STRAIN M732 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7618
STRAIN COH1 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7619
STRAIN M781 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALHESLTGLENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7620
STRAIN CJB110 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7621
STRAIN 1169NT frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALYESLTALENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

SEQ ID NO. 7622
STRAIN JM9130013 frame: 1
KKVIDLKKLQKAYASETVLNNINLEVFKEI IGLIGPSGAGKSTLIKTMLGMEKADKGT
LVLDTQMPDRNINLQIGYMAQSDALYESLTGLENLLFFGKMKGIQKTELKQOITHISKV
DLENQLDKPFVSGYSGGMKRRLSLAIALLGNTVLIIDEPVGDPSLRRKIWQELINIKD
EGRSIFITTHVMDEAELTSKVALLLRGNI IAFDTPLHLKKQFNV

PRETTY of: /biotmp/msa134470.2{*} April 10, 2003 02:16 ..

Table with 4 columns: sequence identifier, alignment position, sequence, and alignment position. It shows a comparison between strain msa134470.2 and various reference sequences (090, A909, H36B, 18RS21, M732, COH1, M781, CJB110, 1169NT, JM9130013) at positions 1 and 50.

Table 76: Comparative Sequences relating to SAG0260

msa134470.2{391_A909}	KKVIDLKKLQ	KAYASETVLN	NINLEVFKE	IIGLIGPSGA	GKSTLIKIML
Consensus	*****	*****	*****	*****	*****
	51				100
msa134470.2{391_090}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_1169NT}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_CJB110}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	aLENLLFFGK
msa134470.2{391_COH1}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M732}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_M781}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALhESLT	gLENLLFFGK
msa134470.2{391_18RS21}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_2603}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_H36B}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_JM9130013}	GMEKADKGT	LVLDTQMPDr	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
msa134470.2{391_A909}	GMEKADKGT	LVLDTQMPDh	NILNQIGYMA	QSDALyESLT	gLENLLFFGK
Consensus	*****	*****	*****	*****	*****
	101				150
msa134470.2{391_090}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_1169NT}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_CJB110}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_COH1}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_M732}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_M781}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_18RS21}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_2603}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_H36B}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_JM9130013}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
msa134470.2{391_A909}	MKGIQKTELK	QQITHISKV	DLENQLDKFV	SGYSGMKRR	LSLAIALLGN
Consensus	*****	*****	*****	*****	*****
	151				200
msa134470.2{391_090}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_1169NT}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_CJB110}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_COH1}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M732}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_M781}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_18RS21}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_2603}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_H36B}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_JM9130013}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
msa134470.2{391_A909}	PTVLILDEPT	VGIDPSLRRK	IWQELINIKD	EGrSIFITTH	VMDEAELTSK
Consensus	*****	*****	*****	**_*****	*****
	201		224		
msa134470.2{391_090}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_1169NT}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_CJB110}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_COH1}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_M732}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_M781}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_18RS21}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_2603}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_H36B}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_JM9130013}	VALLLRGNI	AFDTPLHLKK	QFNV		
msa134470.2{391_A909}	VALLLRGNI	AFDTPLHLKK	QFNV		
Consensus	*****	*****	****		

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7701

STRAIN 2603

TTGCCTAAGTTGCTGTTGGTTTAGTTTTAGAGGGTGGCGGAATGAGAGGCTTTATACT
GCTGGAGTTTTAGATGCTTTTCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTC
TCTGCTGCTGCATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGTTTCGAACA
GGGAATTTTGTAAATAAAGATTTACCTATATGAAAGTTCCTATGAAATGGATGTATTT
GACGATGAAGCAATTTAAAAAATCAAGTATGATTTTTACGTAGTTGCTACAGAGATGACA
TCTGGTAAACCTGAATATTTTAAATTTGATAGTGTTTTTGAAACAAATGGAATTTTACGT
GCTAGTTCAGCATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTTATCTGATAGTATTCCCCTTGATTTTGCCCGTGGTTIAGGATTTGACAAG
TTGATTTGTTGATGACTAGGCCCTCAATATCAGAAAAAGCCTTCAAGTGGACGATTTG
TATAAACTCTGTATAGGAAATATCCTAATTTTGAAGACAGCCTCGAATCGGTACCAA
CAGTATAATAATAGTCTTGAAAAGGTCTAGAGCCTTGAAAAAACAGGCCGATCTATTTGCA
ATTAGACCGAATGAGGCTTGGTTATTTGGCCCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAATAGTTAT
CTAATGAAA

SEQ ID NO. 7702

STRAIN 090

CCTATGTTGCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTLAGATGCTTTT
CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
TTTCGAACAGGGAAATTTGTAAATAAAGATTTACCTATATGAAAGTTC
TATGAAATTTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTG
ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCCTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCCTCAATATCAGAAAAA
GCCCTTCAAGTGGACGATTTGATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAA
AAGGTCTAGAGCCTTGAAAAAACAGGCCGATCTATTTGCAATTAGACCGAG
TAAGAGCTTGGTTATTTGGCCCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7703

STRAIN A909

CCTATGTTGCTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTLAGATGCTTTTCT
AGATGCAGGAATAAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGGCT
TCGAACAGGGAAATTTGTAAATAAAGATTTACCTATATGAAAGTTCCTA
TGAAATTTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTGAT
TTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGCAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTCCCCTTGATTTTGCCCGTGGTTTAGGATT
TGACAAGTTGATTTGTGTGATGACTAGGCCCTCAATATCAGAAAAAGC
CTTCAAGTGGACGATTTGATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAA
GGTCTAGAGCCTTGAAAAAACAGGCCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTTGGCCCTTAGAGAAGAATCCGGATAAACTTGATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

SEQ ID NO. 7704

STRAIN H36B

CCTATGTTGCTGTTGGTTTAGTTTTAG
AGGGTGGCGGAATGAGAGGCTTTTATACTGCTGGAGTTTLAGATGCTTTT
CTAGATGCAGGAATAAAAAGTAGATGGTATCATATCTGCTCTGCTGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCCTAAATATATGAGTCTAAGGTCATGG
CTTCGAACAGGGAAATTTGTAAATAAAGATTTACCTATATGAAAGTTC
TATGAAATTTGGATGTATTTGACGATGAAGCATTAAAAAATCAAGTATTG
ATTTTACGAGTTGCTACAGAGATGACATCTGGTAAACCTGAGTATTTT
AAAATTGATAGTGTTTTTGAACAAATGGAATTTTACGTGCTAGTTTCAGC
ATTACAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTCCCCTTGATTTTGCCCGTGGTTTAGGA
TTTGACAAGTTGATTTGTGTGATGACTAGGCCCTCAATATCAGAAAAA
GCCCTTCAAGTGGACGATTTGATAAACTCTGTATAGGAAATATCCTAATT
TTGTAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAA
AAGGTCTAGAGCCTTGAAAAAACAGGCCGATCTATTTGCAATTAGACCAAG
TAAGAGCTTGGTTATTTGGCCCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTG
AATAGTTATCTAATGAAA

SEQ ID NO. 7705

Table 77: Comparative Sequences relating toSAG2059

STRAIN 18RS21

CCTATGTTGTCTGTTGGTTTAGTTTAGAGG
GTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTTCTA
GATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGCATT
GTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACA
ATAAAAAGTATTTATCCCACCTAANTATATGAGTCTAAGGTCATGGTTT
CGAACAGGGAATTTTGTATAAAGATTTCCACTATTATGAAGTTCCTAT
GAAATGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGATT
TTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAA
ATTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTCAGCATT
ACCAAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATG
GTGGTTTATCTGATAGTATTTCCCGTTGATTTGCCCCGTGGTTTAGGATT
GACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAGCC
TTCAAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTG
TAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAGA
GTCATGAGCCTTGA AAAAACAGCGCATCTATTGCAATTAGACCGAGTAA
GAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAGTA
TTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAAT
AGTTATCTAATGAAA

SEQ ID NO. 7706

STRAIN M732

CCTATGTTGTCTGTTGGTTTAGTTTAGA
GGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTTCT
TAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCA
TTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATA
CAATAAAAAGTATTTATCCCACCTGAATATAAGAGTCTAAGATCATGGC
TTCGAACAGGGAATTTGTTAATAAAGATTTCCACTATTATGAAGTTCCT
ATGAAATTTGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTGA
TTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTA
AAATTTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTCAGCA
TTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGA
TGGTGGTTTATCTGATAGTATTTCCCGTTGATTTGCCCCGTGGTTTAGGAT
TTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAAAG
CCTTCAAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTT
TGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGAAA
AGGTCATGAGCCTTGA AAAAACAGCGCATCTATTGCAATTAGACCGAGT
AAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATAG
TATTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTGA
ATAGTTATCTAATGAAA

SEQ ID NO. 7707

STRAIN COH1

CCTATGTTGTCTGTTGGTTTAGTTTAA
GAGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTT
TCTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTG
CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGGA
TACAATAAAAAGTATTTATCCCACCTGAATATAAGAGTCTAAGATCATG
GCTTCGAACAGGGAATTTGTTAATAAAGATTTCCACTATTATGAAGTTC
CTATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAATTTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTCAG
CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTGCCCCGTGGTTTAGG
ATTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
AGCCTTCAAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGTTCATGAGCCTTGA AAAAACAGCGCATCTATTGCAATTAGACCGA
GTAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGAT
AGTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7708

STRAIN M781

CCTATGTTGTCTGTTGGTTTAGTTTAA
AGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTATAGATGCTTTT
CTAGATGCAGGAATAAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGC
ATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGAT
ACAATAAAAAGTATTTATCCCACCTGAATATAAGAGTCTAAGATCATGG
CTTCGAACAGGGAATTTGTTAATAAAGATTTCCACTATTATGAAGTTC
TATGAAATTTGGATGTATTTGACGATGAAGCATTTAAAAAATCAAGTATTG
ATTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTT
AAAATTTGATAGTGTTTTGAACAAATGGAATTTTACGTGCTAGTTCAGC
ATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAG
ATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTGCCCCGTGGTTTAGGA
TTTGACAAGTTGATTGTTGTGATGACTAGGCCGCTCAATTATCAGAAAA
GCCITCAAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTGTAAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAGGTCATGAGCCTTGA AAAAACAGCGCATCTATTGCAATTAGACCGAG
TAAGAGCTTGGTTATTGGCCGCTTAGAGAAGAATCCGGATAAACTTGATA
GTATTTATCAGCTTGGTATGAAATATGCTAAAAGTGTGATGCCTGAGCTG
AATAGTTATCTAATGAAA

Table 77: Comparative Sequences relating toSAG2059

SEQ ID NO. 7709
STRAIN CJB110
CCTATGTTGTCGTGTTGGTTTAGTTTTA
GAGGGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTTAGATGCTTTT
TCTAGATGCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCTGGTGG
CATTGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGA
TACAATAAAAAGTATTTATCCCACCTAAATATATGAGTCTAAGGTCATG
GTTTCGAAACAGGGAAATTTGTTAATAAAGATTTACCTATTATGAAGTTC
CTATGAAATTTGGATGATTTTGACGATGAAGCATTTAAAAAATCAAGTATT
GATTTTTACGTAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTT
TAAAATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACG
CATTACCAGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTA
GATGGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCTGGTTTAGG
ATTTGACAAGTTGATTGTTTGTGATGACTAGGCCCTCAATTATCAGAAAA
AGCCTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAAT
TTTTGTAAGACAGCCTCGAATCGGTACCAACAGTATAATAATAGTCTTGA
AAAGGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCGA
GTAAGAGCTTGGTTATTTGGCCGCTTAGAGAAGAAATCCGGATAAACCTTGT
AGTATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCT
GAATAGTTATCTAATGAAA

SEQ ID NO. 7710
STRAIN 1169NT
CCTATGTTGTCGTGTTGGTTTAGTTTTAGAGGGTG
GCAGGAATGAGAGGTCCTTATACTGCTGGAGTTTTAGATGCTTTTCTAGAT
GCAGGAATAAAAATAGATGGTATCGTATCTGTCTCTGCGGGTGCATTGTT
TGTTGTTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATACAATA
AAAAGTATTTATCCCACCTAAATATATGAGTCTAAGATCATGGCTTCGA
ACAGGGAATTTTGTAAATAAAGATTTACCTATTTATGAAGTTCCCTATGAA
ATTTGATGATTTTGACGATGAAGCATTTAAAAAATCAAGTATTGATTTTT
ACGCAAGTTGCTACAGAGATGACATCTGGTAAACCTGAATATTTTAAATTT
GATAGTGTCTTTGAACAAATGGAAATTTTACGTGCTAGTTTACGCAATTACC
AGTAGTCTCAAAGATGGTTGATTGGCAGGGGAAAAAGTACTTAGATGGTG
GTTTATCTGATAGTATCCCCTGTTGATTTTGCCTGGTTTAGGATTTGAC
AAGTTGATTGTTGTTGATGACTAGGCCCTCAATTATCAGAAAAAGCCTTC
AAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTTGTAA
AGACAGCCTCGAATCGGTACCAACAGTATAATAATAGCCTTGAAAAGGTC
ATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGGCCGAGTAAAAAG
CTTGGTTATTTGCTCCGCTTAGAGAAGAAATCCGGATAAACCTTGTATAGT
ATCAGCTTGGTATGAAAGATGCTAAAAGTGTGATGCCTGAGCTGAATAGT
TATCTAATGAAA

SEQ ID NO. 7711
STRAIN JM9130013
CCTATGTTGTCGTGTTGGTTTAGTTTTAGAG
GGTGGCGGAATGAGAGGTCCTTATACTGCTGGAGTTTTAGATGCTTTTCT
AGATGCAGGAATAAAGTAGATGGTATCATATCTGTCTCTGCTGGTGCAT
TGTTTGGTGTAAATTTTGTATCTAGACAACGAGAGAGGGCTTTGCGATAC
AATAAAAAGTATTTATCCCACCTAAATATATGAGTCTAAGGTCATGGCT
TCGAAACAGGGAAATTTTGTAAATAAAGATTTACCTATTTATGAAGTTCCCTA
TGAAATTTGATGATTTTGACGATGAAGCATTTAAAAAATCAAGTATTGAT
TTTTACGCAAGTTGCTACAGAGATGACATCTGGTAAACCTGATATTTTAA
AATTGATAGTGTTTTTGAACAAATGGAAATTTTACGTGCTAGTTTACGCAAT
TACCAGTAGTCTCAAAGATGGTTGTTTGGCAGGGGAAAAAGTACTTAGAT
GGTGGTTTATCTGATAGTATTTCCCGTTGATTTTGCCTGGTTTAGGATT
TGACAAGTTGATTTGTTGATGACTAGGCCCTCAATTATCAGAAAAAGC
CTTCAAGTGGACGATTGTATAAACTCTGTATAGGAAATATCCTAATTTT
GTAAAGACAGCCTCGAACCCTGACCAACAGTATAATAATAGCCTTGAAAA
GGTCATGAGCCTTGAAAAAACAGGCGATCTATTTGCAATTAGACCAAGTA
AGAGCTTGGTTATTTGGCCGCTTAGAGAAGAAATCCGGATAAACCTTGTATAGT
ATTTATCAGCTTGGTATGAAAGATGCTAAAAGTGGGATGCCTGAGCTGAA
TAGTTATCTAATGAAA

PRETTY of: /biotmp/maa47199.2{*} February 19, 2003 05:51 ..

Table with 5 columns: Sequence ID, Position 1, Position 51, Position 100, and Consensus. It lists multiple sequence alignments for various strains including msa47199.2 and JM9130013.

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_090}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_18RS21}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_2603}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_CJB110}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_COH1}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M732}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_M781}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
msa47199.2{394_1169NT}	TCTTTATACT	GCTGGAGTTT	TAGATGCTTT	TCTAGATGCA	GGAATAAAAA
Consensus	*****	*****	*****	*****	*****
101					
msa47199.2{394_A909}	TAGATGGTAT	CaTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_H36B}	TAGATGGTAT	CaTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_JM9130013}	TAGATGGTAT	CaTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_090}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_18RS21}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_2603}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_CJB110}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_COH1}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_M732}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_M781}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
msa47199.2{394_1169NT}	TAGATGGTAT	CgTATCTGTC	TCTGctGGTG	CATTGTTTGG	TGTTAAATTTT
Consensus	*****	*-*****	*****-****	*****	*****
151					
msa47199.2{394_A909}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_H36B}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_JM9130013}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_090}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_18RS21}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_2603}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_CJB110}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_COH1}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_M732}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_M781}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
msa47199.2{394_1169NT}	GTATCTAGAC	AACGAGAGAG	GGCITTGCGA	TACAATAAAA	AGTATTTTATC
Consensus	*****	*****	*****	*****	*****
201					
msa47199.2{394_A909}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_H36B}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_JM9130013}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_090}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_18RS21}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_2603}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_CJB110}	CCACCCTaAA	TATATGAGTC	TAAGgTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_COH1}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_M732}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_M781}	CCACCCTgAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GGGAATTTTG
msa47199.2{394_1169NT}	CCACCCTaAA	TATATGAGTC	TAAGaTCATG	GcTTCGAACA	GGGAATTTTG
Consensus	*****-**	*****	*****-*****	*-*****	*****
251					
msa47199.2{394_A909}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_H36B}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_JM9130013}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_090}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_18RS21}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_2603}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_CJB110}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_COH1}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M732}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_M781}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
msa47199.2{394_1169NT}	TTAATAAAGA	TTTCACCTAT	TATGAAGTTC	CTATGAAATT	GGATGTATTT
Consensus	*****	*****	*****	*****	*****
301					
msa47199.2{394_A909}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_H36B}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_JM9130013}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_090}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_18RS21}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_2603}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_CJB110}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_COH1}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_M732}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_M781}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
msa47199.2{394_1169NT}	GACGATGAAG	CATTTAAAAA	ATCAAGTATT	GATTTTTTACG	cAGTTGCTAC
Consensus	*****	*****	*****	*****	-*****
351					
msa47199.2{394_A909}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_H36B}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_JM9130013}	AGAGATGACA	TCTGGTAAAC	CTGAgTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_090}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_18RS21}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_2603}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_CJB110}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_COH1}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M732}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_M781}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTtTTTG
msa47199.2{394_1169NT}	AGAGATGACA	TCTGGTAAAC	CTGAaTATTT	TAAAATTGAT	AGTGTcTTTG
Consensus	*****	*****	***-*****	*****	*****-****
401					
msa47199.2{394_A909}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_H36B}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_JM9130013}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_090}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_18RS21}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_2603}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_CJB110}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_COH1}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M732}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_M781}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
msa47199.2{394_1169NT}	AACAAATGGA	AAITTTACGT	GCTAGTTCAG	CATTACCAGT	AGTCTCAAAG
Consensus	*****	*****	*****	*****	*****
451					
msa47199.2{394_A909}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_H36B}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_JM9130013}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_090}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_18RS21}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_2603}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_CJB110}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_COH1}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M732}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_M781}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
msa47199.2{394_1169NT}	ATGGTTGtTT	GGCAGGGGAA	AAAGTACTTA	GATGGTGGTT	TATCTGATAG
Consensus	*****-*	*****	*****	*****	*****
501					
msa47199.2{394_A909}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_H36B}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_JM9130013}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_090}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_18RS21}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_2603}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_CJB110}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_COH1}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_M732}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_M781}	TATtCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
msa47199.2{394_1169NT}	TATcCCCGTT	GATTTTGCCC	GTGGTTTAGG	ATTTGACAAG	TTGATTGTTG
Consensus	***-*****	*****	*****	*****	*****
551					
msa47199.2{394_A909}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_H36B}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_JM9130013}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_090}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_18RS21}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_2603}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_CJB110}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_COH1}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M732}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_M781}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
msa47199.2{394_1169NT}	TGATGACTAG	GCCGCTCAAT	TATCAGAAAA	AGCCTTCAAG	TGGACGATTG
Consensus	*****	*****	*****	*****	*****
601					
msa47199.2{394_A909}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_H36B}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_JM9130013}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_090}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_18RS21}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_2603}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_CJB110}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_COH1}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M732}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_M781}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
msa47199.2{394_1169NT}	TATAAAACTC	TGTATAGGAA	ATATCCTAAT	TTTGTAAGA	CAGCCTCGAA
Consensus	*****	*****	*****	*****	*****
651					
msa47199.2{394_A909}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAG
700					

Table 77: Comparative Sequences relating toSAG2059

msa47199.2{394_H36B}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_JM9130013}	cCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_090}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_18RS21}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_2603}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_CJB110}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_COH1}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M732}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_M781}	tCGGTACCAA	CAGTATAATA	ATAGtCTTGA	AAAGGTCATG	AGCCTTGAAA
msa47199.2{394_1169NT}	tCGGTACCAA	CAGTATAATA	ATAGcCTTGA	AAAGGTCATG	AGCCTTGAAA
Consensus	*****	*****	****-****	*****	*****
701					
msa47199.2{394_A909}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_H36B}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_JM9130013}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCaA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_090}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_18RS21}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_2603}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_CJB110}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_COH1}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M732}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_M781}	AAACAGGCGA	TCTATTTGCA	ATTAGaCCgA	GTAAGAGCTT	GGTTATTGgC
msa47199.2{394_1169NT}	AAACAGGCGA	TCTATTTGCA	ATTAGgCCgA	GTAaAGCTT	GGTTATTGtC
Consensus	*****	*****	*****-**-*	****-*****	*****-*
751					
msa47199.2{394_A909}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_H36B}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_JM9130013}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_090}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_18RS21}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_2603}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_CJB110}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_COH1}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M732}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_M781}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
msa47199.2{394_1169NT}	CGCTTAGAGA	AGAATCCGGA	TAAACTTGAT	AGTATTTATC	AGCTTGGTAT
Consensus	*****	*****	*****	*****	*****
801					
msa47199.2{394_A909}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_H36B}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_JM9130013}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_090}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_18RS21}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_2603}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_CJB110}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_COH1}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M732}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_M781}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
msa47199.2{394_1169NT}	GAAAgATGCT	AAAAGTgGgA	TGCCTGAGCT	GAATAGTTAT	CTAATGAAA
Consensus	****-*****	*****-*	*****	*****	*****

SEQ ID NO. 7712
 STRAIN 2603 frame: 1
 PMLSVGLVLEGGMRGLYTAGVLDALFDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWFRGTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVAVATEMTS
 GKPEYFKIDSVEFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSI PVDFAFRLGFDKIL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSASNYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7713
 STRAIN 090 frame: 1
 PMLSVGLVLEGGMRGLYTAGVLDALFDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWFRGTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVAVATEMTS
 GKPEYFKIDSVEFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSI PVDFAFRLGFDKIL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSASNYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSVMPPELNSYLMK

SEQ ID NO. 7714
 STRAIN A909 frame: 1
 PMLSVGLVLEGGMRGLYTAGVLDALFDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWFRGTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVAVATEMTS
 GKPEYFKIDSVEFQMEILRASSALPVVSKMVDWQKKYLDGGLSDSI PVDFAFRLGFDKIL
 IVVMTRPLNYQKKPSSGRLYKTLRKYPNFVKTSASNYQQYNNLSLEKVMSEKTDGLFAI
 RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7715
 STRAIN H36B frame: 1
 PMLSVGLVLEGGMRGLYTAGVLDALFDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
 NKKYLSHPKYMSLRSWFRGTGNFVNKDFTYEYVPMKLDVDFDEAFKSSIDFYVAVATEMTS

Table 77: Comparative Sequences relating toSAG2059

GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7716
STRAIN 18RS21 frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7717
STRAIN M732 frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKYAKSVMPPELNSYLMK

SEQ ID NO. 7718
STRAIN COH1 frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKYAKSVMPPELNSYLMK

SEQ ID NO. 7719
STRAIN M781 frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKYAKSVMPPELNSYLMK

SEQ ID NO. 7720
STRAIN CJB110 frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7721
STRAIN JM9130013 frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKVDGII SVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIGRLEKNPKLDSIYQLGMKDAKSGMPELNSYLMK

SEQ ID NO. 7722
STRAIN 1169NT frame: 1
PMLSVGLVLEGGMRGLYTAGVLDNFLDAGIKIDGIVSVSAGALFGVNFVSRQRERALRY
NKKYLSPKYMMSLRSWLRTGNFVNKDFTYEYVPMKLDVDFDEAFKKSIDFYVVAATEMTS
GKPEYFKIDSVFQEIMEILRRASSALPVVSKMVDWQGKKYLDGGLSDSIPVDFARGLGFDKLI
VVMTRPLNYQKKPSSGRLYKTLRYKYPNFVKTAASNRYQQYNNNSLEKVMSELEKTGDLFAI
RPSKSLVIVRLEKNPKLDSIYQLGMKDAKSGMPELNSYLMK

Table with 6 columns: Accession, Position, Consensus, and sequence fragments. Includes entries for msa47322.2 and Consensus sequence.

Table with 6 columns: Accession, Position, Consensus, and sequence fragments. Includes entries for msa47322.2 and Consensus sequence.

Table 77: Comparative Sequences relating toSAG2059

msa47322.2{394_2603}	SRQRERALRY	NKKYLShPKY	MSLRswfRTG	NFVNkdFTYY	EVPmKLDVFD
msa47322.2{394_CjB110}	SRQRERALRY	NKKYLShPKY	MSLRswfRTG	NFVNkdFTYY	EVPmKLDVFD
msa47322.2{394_COH1}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPmKLDVFD
msa47322.2{394_M732}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPmKLDVFD
msa47322.2{394_M781}	SRQRERALRY	NKKYLShPeY	MSLRswlRTG	NFVNkdFTYY	EVPmKLDVFD
Consensus	*****	*****-*	*****-***	*****	*****
101					
msa47322.2{394_A909}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_H36B}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_JM9130013}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_090}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_1169NT}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_18RS21}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_2603}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_CjB110}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_COH1}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_M732}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
msa47322.2{394_M781}	DEAFKkSSID	FyavATEMTS	GKPEYfKIDS	VFEQMEILRA	SSALPvVSKM
Consensus	*****	**-*	*****	*****	*****
151					
msa47322.2{394_A909}	VvWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_H36B}	VvWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_JM9130013}	VvWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_090}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_1169NT}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_18RS21}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_2603}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_CjB110}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_COH1}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_M732}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
msa47322.2{394_M781}	VdWQgkKYLD	GGLSDSIPVD	FARGLGfDKL	IvVMTRPLNY	QKkPSSGRly
Consensus	*-*****	*****	*****	*****	*****
200					
201					
msa47322.2{394_A909}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_H36B}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_JM9130013}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_090}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_1169NT}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_18RS21}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_2603}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_CjB110}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_COH1}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_M732}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
msa47322.2{394_M781}	KTLyRkYPNF	VkTASnRYQQ	YnNSLEkVMS	LEkTGDLFAI	RPSkSLVIgR
Consensus	*****	*****	*****	*****	*****-*
251					
msa47322.2{394_A909}	LEkNPdKLDS	IYQLGmKdAK	SgMPeLNSYL	MK	
msa47322.2{394_H36B}	LEkNPdKLDS	IYQLGmKdAK	SgMPeLNSYL	MK	
msa47322.2{394_JM9130013}	LEkNPdKLDS	IYQLGmKdAK	SgMPeLNSYL	MK	
msa47322.2{394_090}	LEkNPdKLDS	IYQLGmKdAK	SvMPeLNSYL	MK	
msa47322.2{394_1169NT}	LEkNPdKLDS	IYQLGmKdAK	SvMPeLNSYL	MK	
msa47322.2{394_18RS21}	LEkNPdKLDS	IYQLGmKdAK	SvMPeLNSYL	MK	
msa47322.2{394_2603}	LEkNPdKLDS	IYQLGmKdAK	SvMPeLNSYL	MK	
msa47322.2{394_CjB110}	LEkNPdKLDS	IYQLGmKdAK	SvMPeLNSYL	MK	
msa47322.2{394_COH1}	LEkNPdKLDS	IYQLGmKyAK	SvMPeLNSYL	MK	
msa47322.2{394_M732}	LEkNPdKLDS	IYQLGmKyAK	SvMPeLNSYL	MK	
msa47322.2{394_M781}	LEkNPdKLDS	IYQLGmKyAK	SvMPeLNSYL	MK	
Consensus	*****	*****-*	*-*****	**	
282					

Table 78: Comparative Sequences relating to SAG1016

SEQ ID NO. 7801
 STRAIN 2603
 ATGAAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAACGAATTAATTTACCTTCTT
 AATAAGATGATTTCTAACCTCGTTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCT
 ATTTTACTTAGAGAACTTTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTTCT
 GGGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCG
 ACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGATTATTTGTTA
 AAACCCCTATGATTTTATAGGCTAAAGCAAGCTATGGATAGAGTAAAAGGAGCGCTAAGT
 ACATCTCAATATATAGAGAGCGTAACTTCGGTCTCTCTTCAAGCAACAGTATCCATTG
 ACAGTAGAAGATCGAATCTATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATG
 CAAGGAAAACCTGATTATACAAAACCTGATAAAAATTATGAAATGATGGCTCTCTACAA
 CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTTACATTGTG
 AACATTAATGCTATTAACAGGATTGAACCTTGGTTAACCAAACACTTCAGTTACACCTT
 TGTATAAAATAACAGTTCCTGTTAGCAGAGCAATGTAAAACCCCTAAAACAATGTTA
 GGCATATCTACC

SEQ ID NO. 7802
 STRAIN 090
 AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 CGAATTAATTTACCTTCTTAATAAGTATGATTTCTAACCTCGTTATAGCAG
 AGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTT
 GATGTAGCACTGTTAGATATCCATCTCAGAGATGATTTCTGGGTTGCAATT
 AGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGCA
 CTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGAT
 TATTTGTTAAAACCCCTATGATTTTATAGGCTAAAGCAAGCTATGGATAG
 AGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCGG
 GTCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTAT
 CTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAAC
 GATTATACAAACACCTGATAAAAATTATGAAATGATGGCTCTCTACAAC
 AATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCT
 TACATTGTGAACATTAATGCTATTAACAGGATTGAACCTTGGTTAACCA
 AACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAG
 CAATGTAAAACCCCTAAAACAATGTTAGGCATATCTACC

SEQ ID NO. 7803
 STRAIN A909
 AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTTCTAACCTCGTTATAGCAGA
 GCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGCAC
 TGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAAACCCCTATGATTTTATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCGGG
 CCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACCTG
 ATTATACAAAACCTGATAAAAATTATGAAATGATGGCTCTCTACAACA
 ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGACCGCTCTT
 ACATTTGGAATATTAATGCTATTAACAGGATTGAACCTTGGTTAACCA
 ACACCTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAGAGC
 AAATGTAAAACCCCTAAAACAATGTTAGGCATATCTACC

SEQ ID NO. 7804
 STRAIN H36B
 AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTT
 AACGAATTAATTTACCTTCTTAATAAGTATGATTTCTAACCTCGTTATAGC
 AGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTT
 TTGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTTCTGGGTTGCAA
 TTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCG
 GACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTG
 ATTATTTGTTAAAACCCCTATGAGTTTATAGGCTAAAGCAAGCTATGGAT
 AGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTC
 CGGCCCTCTCTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCT
 ATCTGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAA
 CTGATTATACAAAACCTGATAAAAATTATGAAATGATGGCTCTCTACA
 ACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTGACCGCT
 CTTACATTGTGAATATTAATGCTATTAACAGGATTGAACCTTGGTTAAC
 CAAACACTTCAGTTACACCTTTGTAATAAAATAACAGTTCCTGTTAGCAG
 AGCAATGTAAAACCCCTAAAACAATGTTAGGCATATCTACC

SEQ ID NO. 7805
 STRAIN 18RS21
 AAAGTTTTAGTAGTTGATGATGAACCAAGTTGCACGTAAC
 GAATTAATTTACCTTCTTAATAAGTATGATTTCTAACCTCGTTATAGCAGA
 GCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGAGAACTTTT
 ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTTCTGGGTTGCAATTA
 GCAGAGTATATCAATAAAATGCCCAAACCACCATTATTGATATTTGCGCAC
 TGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGATGCGCGTGATT
 ATTTGTTAAAACCCCTATGATTTTATAGGCTAAAGCAAGCTATGGATAGA
 GTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAACTTCGGG
 TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
 TGGTGTGCGCGGATGATATCCTTTTGATTGAAGCTATGCAAGGAAAACCTG

Table 78: Comparative Sequences relating to SAG1016

ATTATACAAAACCTGATAAAAATTATGAAATTTGATGGCTCTCTACAACA
ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
ACATTTGTGAACATTAATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAA
ACACTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCCTGTTAGCAGAGC
AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7806

STRAIN M732

AAAGTTTTAGTAGTTGATGATGAACCCAGTT
GCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGT
TATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTAATTTACTTAGAG
AACTTTTGATGTAGCACGTGTTAGATATCCATCTCAGAGATGATTCTGGG
TTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCCATTATTGAT
ATTCGGCACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATG
CGCGTATTATTGTTAAACCCCTATGAGTTGATAGGTTAAAGCAAGCT
ATGGATAGAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGT
AGCTTCCGGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATC
GAATCTATCTGGTGTGGCGGATGATATCCCTTTTGATTGAAGCTATGCAA
CGAAAACCTGATTATACAAAACCTGATAAAAATTATGAAATTTGATGGCTC
TCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTAC
ATCGCTCTTACATTTGTAATTAATGCTATTAAAAACGATTGAACCTTGG
TTTAAACCAAACCTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCCTGT
TAGCAGAGCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7807

STRAIN COH1

AAAGTTTTAGTAGTTGATGATGAACCCAGTTGCACGTA
ACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCA
GAGGCGCATGATATGGCTACTGCATTAGCTAATTTACTTAGAGAACTTT
TGATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAAT
TAGCAGAGTATATCAATAAAATGCCCAAACCCATTATTGATATTCGGC
ACTGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATGCGCGTGA
TTATTTGTTAAAACCCCTATGAGTTGATAGGTTAAAGCAAGCTATGGATA
GAGTAAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCC
GGTCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTA
TCTGGTGTGGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAAC
TGATTATACAAAACCTGATAAAAATTATGAAATTTGATGGCTCTCTACAA
CAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTC
TTACATTTGTAATTAATGCTATTAAAAACGATTGAACCTTGGTTTAAAC
AAAACCTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCCTGTTAGCAG
GCAAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7808

STRAIN M781

AAAGTTTTAGTAGTTGATGATGAACCCAGTTGCACGTAAC
GAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCGTTATAGCAGA
GGCGCATGATATGGCTACTGCATTAGCTAATTTACTTAGAGAACTTTTG
ATGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGGGTTGCAATTA
GCAGAGTATATCAATAAAATGCCCAAACCCATTATTGATATTCGGCAC
TGCTTATGATCAATATGCTATTTCAGGCTTTTGAGCAGGATGCGCGTGAAT
ATTTGTTAAAACCCCTATGAGTTGATAGGTTAAAGCAAGCTATGGATAGA
GTAAGGAGGCGCTAAGTACATCTACAATTATAGAGAGCGTAGCTTCCGG
TCCTCTCTTCAAGCAACAGTATCCATTGACAGTAGAAGATCGAATCTATC
TGGTGTGGCGGATGATATCCCTTTTGATTGAAGCTATGCAAGGAAACCTG
ATTATACAAAACCTGATAAAAATTATGAAATTTGATGGCTCTCTACAA
ATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTACATCGCTCTT
ACATTTGTAATTAATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAA
ACACTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCCTGTTAGCAGAGC
AAATGTAAAACCCCTAAAACAAATGTTAGGCATATCTACC

SEQ ID NO. 7809

STRAIN CJB110

CTTAATAAGTATGATTCTAACCTCGTTATAGCAGAGGCGCATGATATGGC
TACTGCATTAGCTAATTTACTTAGAGAACTTTTGATGTAGCACTGTTAG
ATATCCATCTCAGAGATGATTCTGGGTTGCAATTAGCAGAGTATATCAAT
AAAATGCCCAAACCCATTATTGATATTTCGGCACTGCTTATGATCAATA
TGCTATTCAAGCTTTTGAGCATGATGCGCGTGAATATTGTTAAAACCCCT
ATGAGTTTGATAGGCTAAAGCAAGTATGGATAGAGTAAAAGGAGCGCTA
AGTACATCTACAATTATAGAGAGCGTAACTTCCGGCCCTCTCTTCAAGCA
ACAGTATCCATTGACAGTAGAAGATnGAATCTATCTGGTGTGGCGGATG
ATATCTCTTTGATTGAAGCTATGCAAGGAAACCTGATTATACAAAACCTT
GATAAAAATTATGAAATTTGATGGCTCTCTACAACAATGGCAAGATAAACT
ACCATCATCTCAATTTGTACGGGTGACCCGCTCTTACATTTGTAATTA
ATGCTATTAAAAACGATTGAACCTTGGTTTAAACCAAACCTTCAGTTACAC
CTTTGTAATAAAAATAACAGTTCCCTGTTAGCAGAGCAAATGTAAAACCCCT
AAAACAAATGTTAGG

SEQ ID NO. 7810

STRAIN 1169NT

AAAGTTTTAGTAGTTGATGATGAACCCAG
TTGCACGTAACGAATTAATTTATCTTCTTAATAAGTATGATTCTAACCTC
GTTATAGCAGAGGCGCATGATATAGCTACTGCATTAGCTAATTTACTTAG

Table 78: Comparative Sequences relating to SAG1016

AGAAACTTTTGTAGTGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTG
GGTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATG
ATATTCCGGCACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGA
TGCGCGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAG
CTATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGC
GTAACCTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAAAGA
TCGAATCTATCTGGTGTGGCGGATGATATCCTTTTGATTGAAGCATGC
AAGGAAAACCTGATTATACAACACCTGATAAAAATTATGAAATTGATGGC
TCTCTACAACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGT
GCACCGCTCTTACATTGTGAATATTAATGCTATTAACACGATTGAACCTT
GGTTTAAACCAAAACACTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCCT
GTTAGCAGAGCAAATGTAAACCCCTAAACAATGTTAGGCATATCTAC
C

SEQ ID NO. 7811

STRAIN JM9130013

AAAGTTTGTAGTGTAGTGTAGTGAACCACT

TGCACGTAACGAATTAATTTACCTTCTTAATAAGTATGATTCTAACCTCG
TTATAGCAGAGGCGCATGATATGGCTACTGCATTAGCTATTTTACTTAGA
GAAACTTTTGTAGTGTAGCACTGTTAGATATCCATCTCAGAGATGATTCTGG
GTTGCAATTAGCAGAGTATATCAATAAAATGCCCAAACCACCATTTATG
TATTCCGGCACTGCTTATGATCAATATGCTATTCAGGCTTTTGAGCATGAT
GCGCGTGATTATTTGTTAAACCCCTATGAGTTTGATAGGCTAAAGCAAGC
TATGGATAGAGTAAAGGAGCGCTAAGTACATCTACAATTATAGAGAGCG
TAACCTCCGGCCCTCTCTTCAAGCAACAGTATCCATTGACAGTAAAGAT
CGAATCTATCTGGGTGTCGGCGGATGATATCCTTTTGATTGAAGCTATGCA
AGGAAAACCTGATTATACAACACCTGATAAAAATTATGAAATTGATGGCT
CTCTACACAATGGCAAGATAAACTACCATCATCTCAATTTGTACGGGTG
CACCGCTCTTACATTGTGAATATTAATGCTATTAACAGATTGAACCTTG
GTTTAAACCAAAACACTTCAGTTACACCTTTGTAATAAAAATAACAGTTCCCTG
TTAGCAGAGCAAATGTAAACCCCTAAACAATGTTAGGCATATCTACC

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa141507.2{*} April 10, 2003 06:36 ..

msa141507.2{399_A909} 1 50
msa141507.2{399_CJB110}
msa141507.2{399_H36B}
msa141507.2{399_JM9130013}
msa141507.2{399_1169NT}
msa141507.2{399_090}
msa141507.2{399_18RS21}
msa141507.2{399_2603}
msa141507.2{399_COH1}
msa141507.2{399_M732}
msa141507.2{399_M781}
Consensus
***-----

msa141507.2{399_A909} 51 100
msa141507.2{399_CJB110}
msa141507.2{399_H36B}
msa141507.2{399_JM9130013}
msa141507.2{399_1169NT}
msa141507.2{399_090}
msa141507.2{399_18RS21}
msa141507.2{399_2603}
msa141507.2{399_COH1}
msa141507.2{399_M732}
msa141507.2{399_M781}
Consensus
-----*** *****

msa141507.2{399_A909} 101 150
msa141507.2{399_CJB110}
msa141507.2{399_H36B}
msa141507.2{399_JM9130013}
msa141507.2{399_1169NT}
msa141507.2{399_090}
msa141507.2{399_18RS21}
msa141507.2{399_2603}
msa141507.2{399_COH1}
msa141507.2{399_M732}
msa141507.2{399_M781}
Consensus
***** ***** ***** ***** *****

msa141507.2{399_A909} 151 200
msa141507.2{399_CJB110}
msa141507.2{399_H36B}
msa141507.2{399_JM9130013}
msa141507.2{399_1169NT}
CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA
CTGTTAGATA TCCATCTCAG AGATGATTCT GGGTTGCAAT TAGCAGAGTA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_090}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_18RS21}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_2603}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_COH1}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M732}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
msa141507.2{399_M781}	CTGTTAGATA	TCCATCTCAG	AGATGATTCT	GGGTTGCAAT	TAGCAGAGTA
Consensus	*****	*****	*****	*****	*****
201					
msa141507.2{399_A909}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_CJB110}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_H36B}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_JM9130013}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_1169NT}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_090}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTtGCG	ACTGCTTATG
msa141507.2{399_18RS21}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTtGCG	ACTGCTTATG
msa141507.2{399_2603}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTtGCG	ACTGCTTATG
msa141507.2{399_COH1}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTtGCG	ACTGCTTATG
msa141507.2{399_M732}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
msa141507.2{399_M781}	TATCAATAAA	ATGCCCAAAC	CACCATTATT	GATATTcGCG	ACTGCTTATG
Consensus	*****	*****	*****	*****_***	*****
251					
msa141507.2{399_A909}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_CJB110}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_H36B}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_JM9130013}	ATCAATATGC	TATTCAaGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_1169NT}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_090}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_18RS21}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_2603}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_COH1}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_M732}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
msa141507.2{399_M781}	ATCAATATGC	TATTCAgGCT	TTTGAGCAtG	ATGCGCGTGA	TTATTTGTTA
Consensus	*****	*****_***	*****_*	*****	*****
301					
msa141507.2{399_A909}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_CJB110}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GnTATGGATA	GAGTAAAAGG
msa141507.2{399_H36B}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_JM9130013}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_1169NT}	AAACCCCTATG	AgTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_090}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_18RS21}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_2603}	AAACCCCTATG	AtTTTGATAG	GcTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_COH1}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_M732}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAAGG
msa141507.2{399_M781}	AAACCCCTATG	AgTTTGATAG	GtTAAAGCAA	GcTATGGATA	GAGTAAAAGG
Consensus	*****	*_*_*_*_*_*_*_*_*	*_*_*_*_*_*_*_*_*	*_*_*_*_*_*_*_*_*	*****
351					
msa141507.2{399_A909}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_CJB110}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_H36B}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_JM9130013}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_1169NT}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGcCCTCTCT
msa141507.2{399_090}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGtCCTCTCT
msa141507.2{399_18RS21}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGtCCTCTCT
msa141507.2{399_2603}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGtCCTCTCT
msa141507.2{399_COH1}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGtCCTCTCT
msa141507.2{399_M732}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGtCCTCTCT
msa141507.2{399_M781}	AGCGCTAAGT	ACATCTACAA	TTATAGAGAG	CGTAaCTTCC	GGtCCTCTCT
Consensus	*****	*****	*****	*****_*****	*****
401					
msa141507.2{399_A909}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_CJB110}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATnGAATCTA	TCTGGTGTCC
msa141507.2{399_H36B}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_JM9130013}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_1169NT}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_090}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_18RS21}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_2603}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_COH1}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_M732}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
msa141507.2{399_M781}	TCAAGCAACA	GTATCCATTG	ACAGTAGAAG	ATcGAATCTA	TCTGGTGTCC
Consensus	*****	*****	*****	**_*_*_*_*_*_*_*_*	*****
451					
msa141507.2{399_A909}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_CJB110}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_H36B}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_JM9130013}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA

Table 78: Comparative Sequences relating to SAG1016

msa141507.2{399_1169NT}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_090}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_18RS21}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_2603}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_COH1}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M732}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
msa141507.2{399_M781}	GCGGATGATA	TCCTTTTGAT	TGAAGCTATG	CAAGGAAAAC	TGATTATACA
Consensus	*****	*****	*****	*****	*****
	501				550
msa141507.2{399_A909}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_CJB110}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_H36B}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_JM9130013}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_1169NT}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_090}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_18RS21}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_2603}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_COH1}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M732}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
msa141507.2{399_M781}	AACACCTGAT	AAAAATTATG	AAATTGATGG	CTCTCTACAA	CAATGGCAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa141507.2{399_A909}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_CJB110}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_H36B}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_JM9130013}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_1169NT}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TgCacCGCTC	TTACATTGTG
msa141507.2{399_090}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_18RS21}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_2603}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_COH1}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M732}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
msa141507.2{399_M781}	ATAAACTACC	ATCATCTCAA	TTTGTACGGG	TaCatCGCTC	TTACATTGTG
Consensus	*****	*****	*****	*_*_*_*_*_*_*_*_*_*	*****
	601				650
msa141507.2{399_A909}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_CJB110}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_H36B}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_JM9130013}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_1169NT}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_090}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_18RS21}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_2603}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_COH1}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_M732}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
msa141507.2{399_M781}	AAtATTAATG	CTATTA AAAAC	GATTGAACTT	TGGTTTAAAC	AAACACTTCA
Consensus	**_*_*_*_*_*_*_*_*_*	*****	*****	*****	*****
	651				700
msa141507.2{399_A909}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_CJB110}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_H36B}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_JM9130013}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_1169NT}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_090}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_18RS21}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_2603}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_COH1}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M732}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
msa141507.2{399_M781}	GTTACACCTT	TGTAATAAAA	TAACAGTTCC	TGTTAGCAGA	GCAAATGTAA
Consensus	*****	*****	*****	*****	*****
	701				732
msa141507.2{399_A909}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_CJB110}	AACCCCTAAA	ACAAATGTTA	GG-----	--	
msa141507.2{399_H36B}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_JM9130013}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_1169NT}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_090}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_18RS21}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_2603}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_COH1}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M732}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
msa141507.2{399_M781}	AACCCCTAAA	ACAAATGTTA	GGcatatcta	cc	
Consensus	*****	*****	*_*_*_*_*_*_*_*_*_*	--	

SEQ ID NO. 7812

STRAIN 2603 frame: 1

KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
LQLAEYINKPKPLLI FATAYDQYAIQAF EHDARDYLLKPYDFDRLKQAMDRVKALST

Table 78: Comparative Sequences relating to SAG1016

STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7813

STRAIN 090 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7814

STRAIN A909 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7815

STRAIN H36B frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7816

STRAIN 18RS21 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7817

STRAIN M732 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7818

STRAIN COH1 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7819

STRAIN M781 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEQDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7820

STRAIN CJB110 frame: 1
 LNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG LQLAEYINKMPKPPLLI F
 ATAYDQYAI QAFEHDARDYLLKPYEFDRLKQXMDRVKALSTSTIIESVTSGLPKQYPL
 TVEDXIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQWQDKLPSSQFVRVHRSYI
 VNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQML

SEQ ID NO. 7821

STRAIN 1169NT frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDIATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

SEQ ID NO. 7822

STRAIN JM9130013 frame: 1
 KVLVVDDEPVARNELIYLLNKYDSNLVIAEAHDMATALA ILLRETFDVALLDIHLRDDSG
 LQLAEYINKMPKPPLLI FATAYDQYAI QAFEHDARDYLLKPYEFDRLKQAMDRVKGALST
 STIIESVTSGLPKQYPLTVEDRIYLVSADDILLI EAMQGKLI I QTPDKNYEIDGSLQQ
 WQDKLPSSQFVRVHRSYIVNINAIKTI EPWFNQTLQLHLCNKITVPVSRANVKPLKQMLG
 IST

Table 78: Comparative Sequences relating to SAG1016

PRETTY of: /biotmp/msa141801.2{*} April 10, 2003 06:38 ..

1 50
msa141801.2{399_COH1} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_M732} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_M781} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_090} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_18RS21} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_2603} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_A909} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_H36B} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_JM9130013} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_1169NT} kvlvvddepv arneliyLLN KYDSNLVIAE AHDmATALAI LLRETFDVAL
msa141801.2{399_CJB110} -----LN KYDSNLVIAE AHDmATALAI LLRETFDVAL
Consensus -----** ***** ***-***** *****

51 100
msa141801.2{399_COH1} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EqDARDYLLK
msa141801.2{399_M732} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EqDARDYLLK
msa141801.2{399_M781} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EqDARDYLLK
msa141801.2{399_090} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_18RS21} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_2603} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_A909} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_H36B} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_JM9130013} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_1169NT} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
msa141801.2{399_CJB110} LDIHLRDDSG LQLAEYINKM PKPPLLIFAT AYDQYAIQAF EhdARDYLLK
Consensus ***** ***** ***** ***** *-*****

101 150
msa141801.2{399_COH1} PYeFDRLKQa MDRVKGALST STIIESVaSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_M732} PYeFDRLKQa MDRVKGALST STIIESVaSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_M781} PYeFDRLKQa MDRVKGALST STIIESVaSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_090} PYdFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_18RS21} PYdFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_2603} PYdFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_A909} PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_H36B} PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_JM9130013} PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_1169NT} PYeFDRLKQa MDRVKGALST STIIESVtSG PLFKQYPLT VEDrIYLVSA
msa141801.2{399_CJB110} PYeFDRLKQx MDRVKGALST STIIESVtSG PLFKQYPLT VEDxIYLVSA
Consensus **-*****- ***** ***** ***** ***** **-*****

151 200
msa141801.2{399_COH1} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_M732} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_M781} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_090} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_18RS21} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_2603} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_A909} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_H36B} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_JM9130013} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_1169NT} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
msa141801.2{399_CJB110} DDILLIEAMQ GKLI IQTPDK NYEIDGSLQQ WQDKLPSSQF VRVHRsYIVN
Consensus ***** ***** ***** ***** ***** *****

201 243
msa141801.2{399_COH1} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_M732} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_M781} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_090} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_18RS21} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_2603} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_A909} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_H36B} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_JM9130013} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_1169NT} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQMLg ist
msa141801.2{399_CJB110} INAIKTIEPW FNQTLQLHLC NKITVPVSRA NVKPLKQML- ---
Consensus ***** ***** ***** ***** - - -

Table 79: Comparative Sequences relating to SAG2150

SEQ ID NO. 7901
 STRAIN 2603
 ATGGGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCCGGCCTCCTTTTGAAGGG
 CGTGCCCTTTTGGACGTCAATCTGAAAATTTGAAGATGCTTCCATACCGCGTTTCATTTGGG
 CACACAGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACA
 AAAGGTGAGGTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATC
 AAATTTATAAGGCAAAAAGTTGGTTAGTTTTCATTTCCAGAAAAGTCAGCTTTTGA
 GAGCAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTGGTATTTCTCAGAITGAA
 GCTGAAAGGCTGGCTGAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGAT
 AAAAAATCCATTTGAACTTTCTGGAGGCGAGATGAGGCGGGTTGCTATAGCTGGTATTTTA
 GCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGA
 AGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTATCGTCTTA
 GTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTATGTGTATGTTTTAGAAGCA
 GGGAAAGTAACTTTATCAGGACAACCAAAACAGATTTTTCAAGAAGTAGAATTTTAGAA
 AGTAAACAATTAGAGATTCCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGA
 TTAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7902
 STRAIN 090
 GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
 GGCCTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAATTTGA
 AGATGCTTCCATACCGCGTTTCATTTGGGCACACAGGTTCTGGAAAATCAA
 CTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
 ATTGTGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAATCAA
 ATTTATAAGGCAAAAAGTTGGTTAGTTTTCATTTCCAGAAAAGTCAGC
 TTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
 GGTATTTCTCAGATTGAAGCTGAAAAGCTGGCTGAAGAAAATTAAGGTT
 AGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTTGAACTTTCTG
 GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
 AAAGTACTAGTACTGGATGAGCCACAGCTGGACTTGATCCTAAGGGGAA
 AAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
 TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTATGCTGACTAT
 GTGTATGTTTTAGAAAGCAGGGAAAGTAACTTTATCAGGACAACCAAAACA
 GATTTTCAAGAAGTAGAACTTTAGAAAAGTAAACAATTAGGAGTTCCCA
 AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAATTTACCT
 AGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7903
 STRAIN A909
 GGAATTGAATTTAAAAATGTAAGTTATACCTATCAA
 GCCGGCACTCCTTTGAAGGGCGTGCCCTTTTGGACGTCAATCTGAAAAT
 TGAAGATGCTTCCATACCGCGTTTCATTTGGGCACACAGGTTCTGGAAAAT
 CAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAG
 GTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACAAGAAAT
 CAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCATTTCCAGAAAAGTC
 AGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACCACAAAAT
 TTTGGTATTTCTCAGATTGAAGCTGAAAAGCTGGCTGAAGAAAATTAAG
 GTTAGTTGGTATCAGTGAGGATTTAATCGATAAAAATCCATTTGAACTTT
 CTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGA
 CCCAAAGTACTAGTACTAGATGAGCCACAGCTGGACTTGATCCTAAGGG
 AAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGA
 CTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTTAGCTGAC
 TATGTGTATGTTTTAGAAGCAGGGAAAGTAACTTTATCAGGACAACCAAA
 GCAGATTTTCAAGAAGTAGAATTTTAAAGTAAACAATTAGGAGTTTCC
 CAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTAATTTA
 CCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTAAGCATGG
 A

SEQ ID NO. 7904
 STRAIN H36B
 GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCCTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC
 TGAAAAATGAAAGATGCTTCCATACCGCGTTTCATTTGGGCACACAGGTTCT
 GGAAAATCAACTATTATGCAACTTTTGAATGGTTTACATATTCCTACAAA
 AGGTGAGGTAATTGTCGATGATTTTCTATTAAAGCAGGGGACAAGAACA
 AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCATTTCCA
 GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGATGTTGCTTTTGGACC
 ACAAATTTTGGTATTTCTCAGATTGAAGCTGAAAAGCTGGCTGAAGAAA
 AATTAAGGTTAGTTGGTATCAGTGAGGATTTAATCGATAAAAATCCATTT
 GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
 GATGGAACCCAAAGTACTAGTACTAGATGAGCCACAGCTGGACTTGATC
 CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAA
 GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
 TGCTGACTATGTGTATGTTTTAGAAGCAGGGAAAGTAACTTTATCAGGAC
 AACCAAGCAGATTTTCAAGAAGTAGAATTTTAAAGTAAACAATTAGGAGTT
 GGAGTTCCCAAAATCACCAGTTTGTCTCAAAGGCTATCTCATAAGGGATTA
 AAATTTACCTAGTTTACCAATTACTATTAAACGAATTTGTGGAGGCTATTA
 AGCATGGA

SEQ ID NO. 7905
 STRAIN 18RS21
 GGAATTGAATTTAAAAATGTAAGTTATAC
 CTATCAAGCCGGCCTCCTTTTGAAGGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATGTTCGATGATTTTCTATTAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCCAAAAGTTGGTTTGTATTTTCAATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTGAAGCAGGGAAAAGTAACCTTATCAGGAC
AACC AAAACAGATTTTCAAGAAGTAGAACCTTTTAGAAAAGTAAACAATTA
GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7906
STRAIN M732

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCCTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC
TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATGTTCGATGATTTTCTATTAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCCAAAAGTTGGTTTGTATTTTCAATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTGAAGCAGGGAAAAGTAACCTTATCAGGAC
AACC AAAACAGATTTTCAAGAAGTAGAACCTTTTAGAAAAGTAAACAATTA
GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7907
STRAIN COH1

GGAATTGAATTTAAAAATGTAAGTTATACCTATCAAGCC
GGCACTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATCTGAAAATGGA
AGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCTGGAAAATCAA
CTATATGCAACTTTTGAATGGTTTACATATTCCTACAAAAGGTGAGGTA
ATGTCGATGATTTTCTATTAAGCAGGGGACAAGAACAAGAAAATCAA
ATTTATAAGGCCAAAAGTTGGTTTGTATTTTCAATTTCCGAAAAGTCAGC
TTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACCACAAAATTTT
GGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAAATTAAGGTT
AGTTGGTATCAGTGAGGATTTATTTCGATAAAAAATCCATTTGAACTTTCTG
GAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGCGATGGAACCC
AAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATCCTAAGGGGAA
AAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAAGGAATGACTA
TCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTTAGCTGACTAT
GTGTATGTTTGAAGCAGGGAAAAGTAACCTTATCAGGACAACCAAAACA
GATTTTCAAGAAGTAGAACCTTTTAGAAAAGTAAACAATTAGGAGTTCCCA
AAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATTAAATTTACCT
AGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTAAGCATGGA

SEQ ID NO. 7908
STRAIN M781

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCCTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC
TGAAAATTGAAGATGTTTCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATATGCAACTTTTGAATGGTTTACATATTCCTACAAA
AGGTGAGGTAATGTTCGATGATTTTCTATTAAGCAGGGGACAAGAACA
AAGAAATCAAATTTATAAGGCCAAAAGTTGGTTTGTATTTTCAATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTAAAGGATGTTGCTTTTGGACC
ACAAAATTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTTCGATAAAAAATCCATTT
GAACTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTTAGC
GATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCTGACTATGTGTATGTTTGAAGCAGGGAAAAGTAACCTTATCAGGAC
AACC AAAACAGATTTTCAAGAAGTAGAACCTTTTAGAAAAGTAAACAATTA
GGAGTTCCCAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7909
STRAIN CJB110

GGAATTGAATTTAAAAATGTAAGTTATAC
CTATCAAGCCGGCCTCCTTTTGAAGGCGTGCCCTTTTGGACGTCAATC

Table 79: Comparative Sequences relating to SAG2150

TGAAAATTGAAGATGCTTCCTATACCGCGTTCATTGGGCACACAGGTTCT
GGAAAATCAACTATTATGCAACTTTTGAATGGTTACATATTCCTACAAA
AGGTGAGTAAATGTGCGATGATTTTCTATTAAGCAGGGGACAAGAAC
AAGAAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCAATTTCCA
GAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTGACC
ACAAAATTTTGGTATTTCTCAGATTGAAAGCTGAAAGGCTGGCTGAAGAAA
AATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAATCCATTT
GAACCTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTTAGC
GATGGAAACCAAGTACTAGTACTGGATGAGCCAACAGCTGGACTTGATC
CTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAAAAAA
GGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGGATTA
TGCAGACTATGTGATGTTTAGAAGCAGGGAAAGTAACCTTATCAGGAC
AACCAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACAATTA
GGAGTTCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGGGATT
AAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCTATTA
AGCATGGA

SEQ ID NO. 7910

STRAIN 1169NT

GGAATTGAATTTAAAAATGTAA
GTTATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGAC
GTCAATCTGAAAATGAAGATGCTTCCTATACCGCGTTCATTGGGCACAC
AGGTTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTACATATTC
CTACAAAAGGTGAGGTAATGTGCGATGATTTTCTATTAAGCAGGGGACA
AAGAACAAAGAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCA
ATTTCCAGAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTT
TTGGACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCT
GAAGAAAATTAAGGTTAGTTGGTATCAGTGAGGATTTATTCGATAAAAA
TCCATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTA
TTTTAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGA
CTTGATCTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCA
TAAAAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAG
CGGATTAATGCTGACTATGTGATGTTTAGAAGCAGGGAAAGTAACCTTA
TCAGGACCAACCAAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAA
ACAATTAGGAGTTCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATA
AGGGATTAAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAG
GCTATTAAGCATGGA

SEQ ID NO. 7911

STRAIN JM9130013

GGAATTGAATTTAAAAATGTAAAGTT
ATACCTATCAAGCCGGCACTCCTTTTGAAGGGCGTGCCCTTTTGGACGTT
AATCTGAAAATGAAGATGCTTCCTATACCGCATTATTGGGCACACAGG
TTCTGGAAAATCAACTATTATGCAACTTTTGAATGGTTACATATTCCTA
CAAAGGTGAGGTAATGTGCGATGATTTTCTATTAAGCAGGGGACAAG
AACAAAGAATCAAATTTATAAGGCAAAAAGTTGGTTAGTTTTCAAT
TCCAGAAAGTCAGCTTTTGAAGAGACAGTTTTAAAGGATGTTGCTTTTG
GACCACAAAATTTTGGTATTTCTCAGATTGAAGCTGAAAGGCTGGCTGAA
GAAAAATTAAGGTTAGTTGGTATTAGTGAGGATTTATTCGATAAAAATCC
ATTTGAACCTTTCTGGAGGGCAGATGAGGCGGGTTGCTATAGCTGGTATTT
TAGCGATGGAACCCAAAGTACTAGTACTGGATGAGCCAACAGCTGGACTT
GATCTAAGGGAAGAAAAGAATTAATGACTCTTTTAAAAATCTTCATAA
AAAAGGAATGACTATCGTCTTAGTGACTCACTTAATGGACGATGTAGCGG
ATTATGCTGACTATGTGATGTTTAGAAGCAGGGAAAGTAACCTTATCA
GGACAACCAAAAACAGATTTTCAAGAAGTAGAAGCTTTAGAAAAGTAAACA
ATTAGGAGTTCCAAAATCACCAGTTTGTCTCAAAGACTATCTCATAAGG
GATTAATTTACCTAGTTTACCAATTACTATTAACGAATTTGTGGAGGCT
ATTAAGCATGGA

PRETTY of: /biotmp/msa238454.2{*} May 14, 2003 06:55 ..

Table with 5 columns: sequence identifier, sequence, position 1, position 50, position 51, position 100. It shows a multiple sequence alignment of various msa238454.2 sequences.

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_COH1}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M732}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_M781}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGtTT
msa238454.2{401_JM9130013}	TTTTGAAGGG	CGTGCCCTTT	TTGACGTcAA	TCTGAAAATT	GAAGATGcTT
Consensus	*****	*****	*****_*	*****	*****_*
101					
msa238454.2{401_A909}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_H36B}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_090}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_1169NT}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_18RS21}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_2603}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_CJB110}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_COH1}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M732}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_M781}	CCTATACCGC	gTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
msa238454.2{401_JM9130013}	CCTATACCGC	aTTCATTGGG	CACACAGGTT	CTGGAAAATC	AACTATTATG
Consensus	*****	*****	*****	*****	*****
151					
msa238454.2{401_A909}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_H36B}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_090}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_1169NT}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_18RS21}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_2603}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_CJB110}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_COH1}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_M732}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_M781}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
msa238454.2{401_JM9130013}	CAACTTTTGA	ATGGTTTACA	TATTCCTACA	AAAGGTGAGG	TAATTGTGCGA
Consensus	*****	*****	*****	*****	*****
201					
msa238454.2{401_A909}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_H36B}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_090}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_1169NT}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_18RS21}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_2603}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_CJB110}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_COH1}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M732}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_M781}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
msa238454.2{401_JM9130013}	TGATTTTTCT	ATTAAAGCAG	GGGACAAGAA	CAAAGAAATC	AAATTTATAA
Consensus	*****	*****	*****	*****	*****
251					
msa238454.2{401_A909}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_H36B}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_090}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_1169NT}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_18RS21}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_2603}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_CJB110}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_COH1}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_M732}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_M781}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
msa238454.2{401_JM9130013}	GGCAAAAAGT	TGGTTTAGTT	TTTCAATTTT	CAGAAAAGTCA	GCTTTTGGAA
Consensus	*****	*****	*****	*****	*****
301					
msa238454.2{401_A909}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_H36B}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_090}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_1169NT}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_18RS21}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_2603}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_CJB110}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_COH1}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_M732}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_M781}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
msa238454.2{401_JM9130013}	GAGACAGTTT	TAAAaGATGT	TGCTTTTGGG	CCACAAAATT	TTGGTATTTT
Consensus	*****	*****	*****	*****	*****
351					
msa238454.2{401_A909}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_H36B}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_090}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_1169NT}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_18RS21}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_2603}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_CJB110}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_COH1}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M732}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_M781}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
msa238454.2{401_JM9130013}	TCAGATTGAA	GCTGAAAGGC	TGGCTGAAGA	AAAATTAAGG	TTAGTTGGTA
Consensus	*****	*****	*****	*****	*****
	401				450
msa238454.2{401_A909}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_H36B}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_090}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_1169NT}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_18RS21}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_2603}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_CJB110}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_COH1}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_M732}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_M781}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
msa238454.2{401_JM9130013}	TcAGTGAGGA	TTTATTCGAT	AAAAATCCAT	TTGAAC TTTC	TGGAGGGCAG
Consensus	*-*****	*****	*****	*****	*****
	451				500
msa238454.2{401_A909}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_H36B}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_090}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_1169NT}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_18RS21}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_2603}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_CJB110}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_COH1}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M732}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_M781}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
msa238454.2{401_JM9130013}	ATGAGGCGGG	TTGCTATAGC	TGGTATTTTA	GCGATGGAAC	CCAAAGTACT
Consensus	*****	*****	*****	*****	*****
	501				550
msa238454.2{401_A909}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_H36B}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_090}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_1169NT}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_18RS21}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_2603}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_CJB110}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_COH1}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M732}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_M781}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
msa238454.2{401_JM9130013}	AGTACTgGAT	GAGCCAACAG	CTGGACTTGA	TCCTAAGGGA	AGAAAAGAAT
Consensus	*****-***	*****	*****	*****	*****
	551				600
msa238454.2{401_A909}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_H36B}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_090}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_1169NT}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_18RS21}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_2603}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_CJB110}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_COH1}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M732}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_M781}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
msa238454.2{401_JM9130013}	TAATGACTCT	TTTTAAAAAT	CTTCATAAAA	AAGGAATGAC	TATCGTCTTA
Consensus	*****	*****	*****	*****	*****
	601				650
msa238454.2{401_A909}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_H36B}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_090}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_1169NT}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_18RS21}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_2603}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_CJB110}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_COH1}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M732}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_M781}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
msa238454.2{401_JM9130013}	GTGACTCACT	TAATGGACGA	TGTAGCGGAT	TATGCTGACT	ATGTGTATGT
Consensus	*****	*****	*****	*****	*****
	651				700
msa238454.2{401_A909}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTTC
msa238454.2{401_H36B}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAag	CAGATTTTTTC
msa238454.2{401_090}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC
msa238454.2{401_1169NT}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC
msa238454.2{401_18RS21}	TTTGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAa	CAGATTTTTTC

Table 79: Comparative Sequences relating to SAG2150

msa238454.2{401_2603}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTTC
msa238454.2{401_CJB110}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTTC
msa238454.2{401_COH1}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTTC
msa238454.2{401_M732}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTTC
msa238454.2{401_JM9130013}	TTTAGAAGCA	GGGAAAGTAA	CCTTATCAGG	ACAACCAAAa	CAGATTTTTTC
Consensus	*****	*****	*****	*****	*****
	701				750
msa238454.2{401_A909}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_H36B}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_090}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_1169NT}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_18RS21}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_2603}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_CJB110}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_COH1}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M732}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_M781}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
msa238454.2{401_JM9130013}	AAGAAGTAGA	ACTTTTAGAA	AGTAAACAAT	TAGGAGTTCC	CAAAATCACC
Consensus	*****	*****	*****	*****	*****
	751				800
msa238454.2{401_A909}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_H36B}	AAGTTTGCTC	AAAGgCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_090}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_1169NT}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_18RS21}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_2603}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_CJB110}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_COH1}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M732}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_M781}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
msa238454.2{401_JM9130013}	AAGTTTGCTC	AAAGaCTATC	TCATAAGGGA	TTAAATTTAC	CTAGTTTACC
Consensus	*****	*****	*****	*****	*****
	801				840
msa238454.2{401_A909}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_H36B}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_090}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_1169NT}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_18RS21}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_2603}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_CJB110}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_COH1}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M732}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_M781}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
msa238454.2{401_JM9130013}	AATTACTATT	AACGAATTTG	TGGAGGCTAT	TAAGCATGGA	
Consensus	*****	*****	*****	*****	

SEQ ID NO. 7912
 STRAIN 2603 frame: 1
 MGIEFKNVSYTYQAGTPEFGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVI VDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPNFGISQIEA
 ERLAEKRLRVGISSEDLFDKNPFELSGGQMRVVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKHLHKKGMTIVLVTHLMDDVDVADYVYVLEAGKVTLGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7913
 STRAIN 090 frame: 1
 GIEFKNVSYTYQAGTPEFGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVI VDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPNFGISQIEA
 ERLAEKRLRVGISSEDLFDKNPFELSGGQMRVVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKHLHKKGMTIVLVTHLMDDVDVADYVYVLEAGKVTLGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7914
 STRAIN 090 frame: 1
 GIEFKNVSYTYQAGTPEFGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVI VDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPNFGISQIEA
 ERLAEKRLRVGISSEDLFDKNPFELSGGQMRVVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKHLHKKGMTIVLVTHLMDDVDVADYVYVLEAGKVTLGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7915
 STRAIN H36B frame: 1
 GIEFKNVSYTYQAGTPEFGRALFDVNLKIEDASYTAFIGHTGSGKSTIMQLLNGLHIPTK
 GEVI VDDFSIKAGDKNKEIKFIRQKVGLVFQFPESQLFEETVLKDVAFGPNFGISQIEA
 ERLAEKRLRVGISSEDLFDKNPFELSGGQMRVVAIAGILAMEPKVLVLDEPTAGLDPKGR
 KELMTLFLKHLHKKGMTIVLVTHLMDDVDVADYVYVLEAGKVTLGQPKQIFQEVVELLES
 KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7916

Table 79: Comparative Sequences relating to SAG2150

STRAIN 18RS21 frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDASYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7917
STRAIN M732 frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDVSYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7918
STRAIN COH1 frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDVSYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7919
STRAIN M781 frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDVSYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7920
STRAIN CJB110 frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDASYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7921
STRAIN 1169NT frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDASYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

SEQ ID NO. 7922
STRAIN JM9130013 frame: 1
GIEFKNVSYTYQAGTFFEGRALFDVNLKIEDASYTAFI GHTGSGKSTIMQLLNLGLHIPTK
GEVIVDDFSIKAGDKNKEIKFIRQKVGLVVFQFPESQLFEETVLKDVAFGPNFGISQIEA
ERLAEEKRLRLVIGISEDLFDKNPFELSGGQMRRAIAGILAMEPKVLVLDEPTAGLDPKGR
KELMTLTFKNLHKKGMTIVLVTHLMDDVDADYADYVYVLEAGKVTLSGQPKQIFQEVLELLES
KQLGVPKITKFAQRLSHKGLNLPSPITINEFVEAIKHG

PRETTY of: /biotmp/msa238553.2{*} May 14, 2003 06:55 ..

1 50
msa238553.2{401_090} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_1169NT} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_18RS21} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_2603} mGIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_CJB110} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_H36B} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_JM9130013} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDaSYTAFIG HTGSGKSTIM
msa238553.2{401_COH1} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
msa238553.2{401_M732} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM
msa238553.2{401_M781} ~GIEFKNVSY TYQAGTFFEG RALFDVNLKI EDvSYTAFIG HTGSGKSTIM

Consensus ***** **_***** *****

51 100
msa238553.2{401_090} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_1169NT} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_18RS21} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_2603} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_CJB110} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_H36B} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_JM9130013} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_COH1} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_M732} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE
msa238553.2{401_M781} QLLNGLHIPT KGEVIVDDFS IKAGDKNKEI KFIRQKVGLV FQFPESQLFE

Table 79: Comparative Sequences relating to SAG2150

Consensus	*****	*****	*****	*****	*****
	101				150
msa238553.2{401_090}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_1169NT}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_18RS21}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_2603}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_CJB110}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_H36B}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_JM9130013}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_COH1}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M732}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
msa238553.2{401_M781}	ETVLKDVAFG	PQNFGISQIE	AERLAEEKLR	LVGISEDLF	KNPFELSGGQ
Consensus	*****	*****	*****	*****	*****
	151				200
msa238553.2{401_090}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_1169NT}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_18RS21}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_2603}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_CJB110}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_H36B}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_JM9130013}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_COH1}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_M732}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
msa238553.2{401_M781}	MRRVAIAGIL	AMEPKVLVLD	EPTAGLDPKG	RKELMTLFPK	LHKKGMTIVL
Consensus	*****	*****	*****	*****	*****
	201				250
msa238553.2{401_090}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_1169NT}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_18RS21}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_2603}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_CJB110}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_H36B}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_JM9130013}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_COH1}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_M732}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
msa238553.2{401_M781}	VTHLMDDVAD	YADYVYVLEA	GKVTLGQPK	QIFQEVLEL	SKQLGVPKIT
Consensus	*****	*****	*****	*****	*****
	251				280
msa238553.2{401_090}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_1169NT}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_18RS21}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_2603}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_CJB110}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_H36B}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_JM9130013}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_COH1}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M732}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
msa238553.2{401_M781}	KFAQRLSHKG	LNLPSLPITI	NEFVEAIKHG		
Consensus	*****	*****	*****		

Table 80: Comparative Sequences relating to SAG1266

SEQ ID NO. 8001
 STRAIN 2603
 GTGAACCCACTTACTTAACCTCAGTAAAGAAAATATAGCTAAAATAGATTTTGACTTTCTT
 AATGAGGCACCTAATGCAAAATATTCGTTTGAAGAAGATAGTAGATGAACATAAAAATTTCA
 AAAGAAGTGGACAGTAAAGGTTGGTCCAAAAAGACTCTCGAACGATAAAAATCTTGTAC
 GATGGCCTTATCAATAAACAATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCAA
 GTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAAGGGAGAATTCT
 AAAAAATTATAGAAATATACAACTACAGTGATTATGAAATGGAGTTAATCAATGAGGATAGG
 CAACAATTTTCAAAATATGAAAACAGTTGATTTAGACCAATTGATACTTGTGTATATTTT
 AATATTGATGACTACATTTTCATCATATTTAACAATA

SEQ ID NO. 8002
 STRAIN H36B
 AACCACTTACTTAACCTCAGTAAAGAAAATATAGCT
 AAAATAGATTTTGACTTTCTTAATGAGGCACCTAATGCAAAATATTCGTTT
 GAAAGAATTAGTAGATGAACATAAAAATTTCAAAGAAGTGGACAGTAAAG
 GTTGGTCCAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCCTT
 ATCAATAAACAATATAGTTTCCCTAGATCGTGCAGATTATAACATTATCCA
 AGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGAAA
 GGGAGAATTCTAAAATATATAGAAATATACAACTACAGTGATTATGAAATG
 GAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAAACAGTTGA
 TTTAGACCAATTGATACTTGTGTATATTTAATAATTGATGACTACATTT
 CATCATATTTAACAATA

SEQ ID NO. 8003
 STRAIN 18RS21
 AACCACTTACTTAACCTCAGTAAAGAAAATATAG
 CTAATAATAGATTTTGACTTTCTTAATGAGGCACCTAATGCAAAATATTCGTT
 TTGAAAGAAATAGTAGATGAACATAAAAATTTCAAAGAAGTGGACAGTAA
 AGGTTGGTCCAAAAAGACTCTCGAACGATAAAAATCTTGTACGATGGCCTT
 TTATCAATAAACAATATAGTTTCCCTAGATCGTGCAGATTATAACATTATC
 CAAGTCATTCCATTTGCTAATGTACATGTACTACTGTTTTTAATACCAGA
 AAGGGAGAAATCTAAAATATATAGAAATATACAACTACAGTGATTATGAAA
 TGGAGTTAATCAATGAGGATAGGCAACAATTTTCAAAATATGAAAACAGTT
 GATTTAGACCAATTGATACTTGTGTATATTTAATAATTGATGACTACAT
 TTCATCATATTTAACAATA

PRETTY of: /biotmp/msa49308.2{*} February 19, 2003 07:45 ..

	1				50
msa49308.2{408_18RS21}	---AACCACT	TACTTAACCT	CAGTAAAGAA	AATATAGCTA	AAATAGATTT
msa49308.2{408_2603}	gtgAACCACT	TACTTAACCT	CAGTAAAGAA	AATATAGCTA	AAATAGATTT
msa49308.2{408_H36B}	---AACCACT	TACTTAACCT	CAGTAAAGAA	AATATAGCTA	AAATAGATTT
Consensus	*****	*****	*****	*****	*****
	51				100
msa49308.2{408_18RS21}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA	TATTCGTTTG	AAAGAATTAG
msa49308.2{408_2603}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA	TATTCGTTTG	AAAGAATTAG
msa49308.2{408_H36B}	TGACTTTCTT	AATGAGGCAC	TTAATGCAAA	TATTCGTTTG	AAAGAATTAG
Consensus	*****	*****	*****	*****	*****
	101				150
msa49308.2{408_18RS21}	TAGATGAACT	AAAAATTTCA	AAAGAACTGG	ACAGTAAAGG	TTGGTCCAAA
msa49308.2{408_2603}	TAGATGAACT	AAAAATTTCA	AAAGAACTGG	ACAGTAAAGG	TTGGTCCAAA
msa49308.2{408_H36B}	TAGATGAACT	AAAAATTTCA	AAAGAACTGG	ACAGTAAAGG	TTGGTCCAAA
Consensus	*****	*****	*****	*****	*****
	151				200
msa49308.2{408_18RS21}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC	GATGGCCTTA	TCAATAAACA
msa49308.2{408_2603}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC	GATGGCCTTA	TCAATAAACA
msa49308.2{408_H36B}	AAAGACTCTC	GAACGATAAA	AATCTTGTAC	GATGGCCTTA	TCAATAAACA
Consensus	*****	*****	*****	*****	*****
	201				250
msa49308.2{408_18RS21}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA	CATTATCCAA	GTCATTCCAT
msa49308.2{408_2603}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA	CATTATCCAA	GTCATTCCAT
msa49308.2{408_H36B}	TATAGTTTCC	CTAGATCGTG	CAGATTATAA	CATTATCCAA	GTCATTCCAT
Consensus	*****	*****	*****	*****	*****
	251				300
msa49308.2{408_18RS21}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA	TACCAGAAAG	GGAGAATTCT
msa49308.2{408_2603}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA	TACCAGAAAG	GGAGAATTCT
msa49308.2{408_H36B}	TTGCTAATGT	ACATGTACTA	CTGTTTTTAA	TACCAGAAAG	GGAGAATTCT
Consensus	*****	*****	*****	*****	*****
	301				350
msa49308.2{408_18RS21}	AAAAATTATA	GAATATACAA	CTACAGTGAT	TATGAAATGG	AGTTAATCAA
msa49308.2{408_2603}	AAAAATTATA	GAATATACAA	CTACAGTGAT	TATGAAATGG	AGTTAATCAA
msa49308.2{408_H36B}	AAAAATTATA	GAATATACAA	CTACAGTGAT	TATGAAATGG	AGTTAATCAA
Consensus	*****	*****	*****	*****	*****

Table 80: Comparative Sequences relating to SAG1266

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351                                     400
msa49308.2{408_18RS21} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_2603} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
msa49308.2{408_H36B} TGAGGATAGG CAACAATTTT CAAAATATGA AACAGTTGAT TTAGACCAAT
Consensus *****

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401                                     450
msa49308.2{408_18RS21} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_2603} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
msa49308.2{408_H36B} TGATACTTGT TGATATTTT AATATTGATG ACTACATTTC ATCATATTTA
Consensus *****

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451
msa49308.2{408_18RS21} ACAATA
msa49308.2{408_2603} ACAATA
msa49308.2{408_H36B} ACAATA
Consensus *****

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SEQ ID NO. 8004

STRAIN 2603 frame: 1

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VNHLNLSKENIAKIDFDLNEALNANIRLDELKISKELDSKGWSKDSRTIKILY
DGLINKHIVSLDRADYNIQVIPPANVHVLFLIPERENSKNYRIYNYSYEMELINEDR
QQFSKYETVLDLQILVDIFNIDDISSYLTI

```

SEQ ID NO. 8005

STRAIN H36B frame: 1

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NHLLNLSKENIAKIDFDLNEALNANIRLDELKISKELDSKGWSKDSRTIKILYD
GLINKHIVSLDRADYNIQVIPPANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVLDLQILVDIFNIDDISSYLTI

```

SEQ ID NO. 8006

STRAIN 18RS21 frame: 1

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NHLLNLSKENIAKIDFDLNEALNANIRLDELKISKELDSKGWSKDSRTIKILYD
GLINKHIVSLDRADYNIQVIPPANVHVLFLIPERENSKNYRIYNYSYEMELINEDRQ
QQFSKYETVLDLQILVDIFNIDDISSYLTI

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PRETTY of: /biotmp/msa49418.2{*} February 19, 2003 07:47 ..

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1                                     50
msa49418.2{408_18RS21} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_2603} vNHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
msa49418.2{408_H36B} -NHLLNLSKE NIAKIDFDL NEALNANIRL KELVDELKIS KELDSKGWSK
Consensus *****

```

```

51                                     100
msa49418.2{408_18RS21} KDSRTIKILY DGLINKHIVS LDRADYNIQ VIPANVHVL LFLIPERENS
msa49418.2{408_2603} KDSRTIKILY DGLINKHIVS LDRADYNIQ VIPANVHVL LFLIPERENS
msa49418.2{408_H36B} KDSRTIKILY DGLINKHIVS LDRADYNIQ VIPANVHVL LFLIPERENS
Consensus *****

```

```

101                                    150
msa49418.2{408_18RS21} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_2603} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
msa49418.2{408_H36B} KNYRIYNYS YEMELINEDR QQFSKYETVD LDQLILVDIF NIDDISSYL
Consensus *****

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151
msa49418.2{408_18RS21} TI
msa49418.2{408_2603} TI
msa49418.2{408_H36B} TI
Consensus **

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Table 81: Comparative Sequences relating to SAG0011

SEQ ID NO. 8101

STRAIN 090

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAGAAAGTTGTAATAATTAACGAAAGACTATCAGACAT
TAACATAAGAACTGAGAACCAGAAGTTGCTAGCAAAACAATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTTTCTCTAAGAC
CGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8102

STRAIN A909

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATA
TATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCG
TTTAAATGGGTTGGGTTCTTATTTTGTTCATGCTtttATTTATTTTACCCTTATAATTT
AGTTAAGAGTTACAGAACTTTACAAGAACGTCGTCAGAAAGTTGTAATAATTAACGAAAGA
CTATCAGACATTAACATAAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAA
TCCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTTTCTCTAAGACCGCGAAAT
GATTTACCCATTACCAGACCT

SEQ ID NO. 8103

STRAIN H36B

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAGAAAGTTGTAATAATTAACGAAAGACTATCAGACAT
TAACATAAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTTTCTCTAAGAC
CGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8104

STRAIN 18RS21

AGCAAGCCTAATGTTGTTTCAGTTAAATAATCAATATATTAACGATGAGAATCTAAAAAAA
CGTTACGAAGCTGAGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTT
GTTCATGCTTTTATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAACTTTACAA
GAACGTCGTCAGAAAGTTGTAATAATTAACGAAAGACTATCAGACATTAACATAAGAACT
GAGAACCAGAAGTTGCTAGCAAAACAATAAAAAATCCAGATTACGTTCAAAAATATGCT
CGAGCTAAGTATTTTCTCTAAGACCGCGAAATGATTTACCCATTACCAGACCTTTTAC
CAAAA

SEQ ID NO. 8105

STRAIN M732

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATG
CTTTTATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAACTTT
ACAAGAACGTCGTCAGAAAGTTGTAATAATTAACGAAAGACTATCAGACAT
TAACATAAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGGAAAGTATTTTCTCTAAGAC
CGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8106

STRAIN COH1

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATGCTttt
ATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG
AACGTCGTCAGAAAGTTGTAATAATTAACGAAAGACTATCAGACATTAAC
AATAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCGAAGTATTTTCTCTAAGACCGCG
AAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8107

STRAIN M781

AGCaAGCCTAATGTTGTTTCAGTT
AAATAATCAATATaTTAACGATGAGAATCTAAAAAACGTTACGAAGCTG
AGGAGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTC
ATGCTTTTATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAAC
TTTACAAGAACGTCGTCAGAAAGTTGTAATAATTAACGAAAGACTATCAGA
CATTAACATAAGAACTGAGAACCAGAAGTTACTAGCAAAACAATAAAAA
AATCCAGATTACGTTCAAAAATATGCTCGAGCGAAGTATTTTCTCTAA
GACCGCGAAATGATTTACCCATTACCAGACCTTTTACCAAAA

SEQ ID NO. 8108

STRAIN CJB110

AGCAAGCCTAATGTTGTTTCAGTTAAATAATC
AATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGGAGTTA
CGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTTCATGCTttt
ATTTATTTTACCCTTATAATTTAGTTAAGAGTTACAGAACTTTACAAG

Table 81: Comparative Sequences relating to SAG0011

AACGTCGTCAAGAAGTTGTAATAAATAACGAAAGACTATCAGACATTAAC
AATAGAAGTGAAGACCAGAAGTTGCTAGCAAACAACTAAAAATCCAGA
TTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCTCTAAGACCGGGG
AAATGATTTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8109

STRAIN 1169NT

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
ACAAGAAGCTCGTCAAGAAGTTGTAATAAATAACGAAAGACTATCAGACAT
TAACATAATAGAAGTGAAGACCAGAAGTTACTAGCAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCTCTAAGAC
CGCGAAATGATTTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8110

STRAIN JM9130013

AGCAAGCCTAATGTTGTTTCAGTTAAA
TAATCAATATATTAACGATGAGAATCTAAAAAACGTTACGAAGCTGAGG
AGTTACGCCGAAAAAATCGTTTAAATGGGTTGGGTTCTTATTTTGTCTATG
CTTTTATTTATTTTACCCACTTATAATTTAGTTAAGAGTTACAGAACCTTT
ACAAGAAGCTCGTCAAGAAGTTGTAATAAATAACGAAAGACTATCAGACAT
TAACATAATAGAAGTGAAGACCAGAAGTTACTAGCAAACAACTAAAAAAT
CCAGATTACGTTCAAAAATATGCTCGAGCTAAGTATTATTCTCTAAGAC
TGGCGAAATGATTTACCCATTACCAGACCTTTACCAAAA

SEQ ID NO. 8111

STRAIN 2603

agcaagcctaagtgttcagttaataatcaatataattaacgatgagaa
tctaaaaaacgttacgaagctgaggagtacgccgaaaaaatcgtttaa
tgggttgggttctctattttgtcatgcttttattttaccacttat
aattagttaagagttacagaactttacaagaagctcgtcaagaagttgt
aaaataacgaagactatcagacattaactaatagaactgagaaccaga
agttgctagcaaaacaactaaaaatccagattacgttcaaaaatagct
cgagctaagattatttctctaagaccgycgaatgatattaccattacc
agaccttttaccaaaa

PRETTY of: /biotmp/msa25643.2(*) . April 29, 2002 05:59 ..

Table with 6 columns of sequence data. Row 1: msa25643.2{418_COH1} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 2: msa25643.2{418_M732} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 3: msa25643.2{418_M781} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 4: msa25643.2{418_JM9130013} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 5: msa25643.2{418_090} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 6: msa25643.2{418_18RS21} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 7: msa25643.2{418_2603} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 8: msa25643.2{418_CJB110} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 9: msa25643.2{418_1169NT} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 10: msa25643.2{418_A909} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 11: msa25643.2{418_H36B} AGCAAGCCTA ATGTTGTTCA GTTAAATAAT CAATATATTA ACGATGAGAA. Row 12: Consensus *****

Table with 6 columns of sequence data. Row 1: msa25643.2{418_COH1} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 2: msa25643.2{418_M732} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 3: msa25643.2{418_M781} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 4: msa25643.2{418_JM9130013} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 5: msa25643.2{418_090} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 6: msa25643.2{418_18RS21} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 7: msa25643.2{418_2603} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 8: msa25643.2{418_CJB110} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 9: msa25643.2{418_1169NT} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 10: msa25643.2{418_A909} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 11: msa25643.2{418_H36B} TCTAAAAAAA CGTTACGAAG CTGAGGAGTT ACGCCGAAAA AATCGTTTAA. Row 12: Consensus *****

Table with 6 columns of sequence data. Row 1: msa25643.2{418_COH1} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 2: msa25643.2{418_M732} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 3: msa25643.2{418_M781} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 4: msa25643.2{418_JM9130013} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 5: msa25643.2{418_090} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 6: msa25643.2{418_18RS21} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 7: msa25643.2{418_2603} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 8: msa25643.2{418_CJB110} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 9: msa25643.2{418_1169NT} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 10: msa25643.2{418_A909} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 11: msa25643.2{418_H36B} TGGGTTGGGT TCTTATTTT GTCATGCTTT TATTTATTTT ACCCACTTAT. Row 12: Consensus *****

Table 81: Comparative Sequences relating to SAG0011

	151				200
msa25643.2{418_COH1}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M732}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_M781}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_JM9130013}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_090}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_18RS21}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_2603}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_CJB110}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_1169NT}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_A909}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
msa25643.2{418_H36B}	AATTTAGTTA	AGAGTTACAG	AACTTTACAA	GAACGTCGTC	AAGAAGTTGT
Consensus	*****	*****	*****	*****	*****
	201				250
msa25643.2{418_COH1}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M732}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_M781}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_JM9130013}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_090}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_18RS21}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_2603}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_CJB110}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_1169NT}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_A909}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
msa25643.2{418_H36B}	AAAATTAACG	AAAGACTATC	AGACATTAAC	TAATAGAACT	GAGAACCAGA
Consensus	*****	*****	*****	*****	*****
	251				300
msa25643.2{418_COH1}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M732}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_M781}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_JM9130013}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_090}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_18RS21}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_2603}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_CJB110}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_1169NT}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_A909}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
msa25643.2{418_H36B}	AGTTACTAGC	AAAACAACCTA	AAAAATCCAG	ATTACGTTCA	AAAATATGCT
Consensus	****-****	*****	*****	*****	*****
	301				350
msa25643.2{418_COH1}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M732}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_M781}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_JM9130013}	CGAGCgAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_090}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_18RS21}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_2603}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_CJB110}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_1169NT}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_A909}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
msa25643.2{418_H36B}	CGAGCtAAGT	ATTATTTCTC	TAAGACcGGC	GAAATGATTT	ACCCATTACC
Consensus	*****-****	*****	*****-****	*****	*****
	351		366		
msa25643.2{418_COH1}	AGACCTttta	ccaaaa			
msa25643.2{418_M732}	AGACCTttta	ccaaaa			
msa25643.2{418_M781}	AGACCTttta	ccaaaa			
msa25643.2{418_JM9130013}	AGACCTttta	ccaaaa			
msa25643.2{418_090}	AGACCTttta	ccaaaa			
msa25643.2{418_18RS21}	AGACCTttta	ccaaaa			
msa25643.2{418_2603}	AGACCTttta	ccaaaa			
msa25643.2{418_CJB110}	AGACCTttta	ccaaaa			
msa25643.2{418_1169NT}	AGACCTttta	ccaaaa			
msa25643.2{418_A909}	AGACCT----	-----			
msa25643.2{418_H36B}	AGACCTttta	ccaaaa			
Consensus	*****----	-----			

SEQ ID NO. 8112
 STRAIN 090
 SKPNVVQLNNQYINDENLKKRYEABBLRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM
 IYPLDLLPK

SEQ ID NO. 8113
 STRAIN A909
 SKPNVVQLNNQYINDENLKKRYEABBLRRKNRLMGWVLI FVMLLFILPTYNL
 VKSYRTLQERRQEVVVKLTKDYQTLTNRTENQKLLAKQLKNPDYVQKYARAKYFYSKTGEM

Table 81: Comparative Sequences relating to SAG0011

IYPLPD

SEQ ID NO. 8114

STRAIN H36B

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKS YRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
IYPLPDLLPK

SEQ ID NO. 8115

STRAIN 18RS21

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKS YRTLQ
ERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IYPLD
LLPK

SEQ ID NO. 8116

STRAIN M732

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKS YRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
IYPLPDLLPK

SEQ ID NO. 8117

STRAIN COH1

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
SYRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IY
PLPDLLPK

SEQ ID NO. 8118

STRAIN M781

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYN
LVKS YRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGE
MIYPLPDLLPK

SEQ ID NO. 8119

STRAIN CJB110

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVK
SYRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IY
PLPDLLPK

SEQ ID NO. 8120

STRAIN 1169NT

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKS YRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
IYPLPDLLPK

SEQ ID NO. 8121

STRAIN JM9130013

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNL
VKS YRTLQERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM
IYPLPDLLPK

SEQ ID NO. 8122

STRAIN 2603

SKPNVVQLNNQYINDENLKKRYEAEELRRKNRLMGWVLI FVMLLFILPTYNLVKS YRTLQ
ERRQEVVVKLT KDYQTLTNR TENQKLLAKQLKNPDYVQKYARAKYF SKTGEM IYPLD
LLPK

MSA Alignment Results: Pretty output

PRETTY of: /biotmp/msa20122.2{*} April 29, 2002 06:08 ..

Table with 2 columns: sequence identifiers (e.g., msa20122.2{418_090}) and sequence alignments. Includes a consensus line and a second alignment section at the bottom.

Table 81: Comparative Sequences relating to SAG0011

msa20122.2{418_1169NT}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_18RS21}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_2603}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_CJB110}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_COH1}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_H36B}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_JM9130013}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M732}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
msa20122.2{418_M781}	NLVKSYRTLQ	ERRQEVVKLT	KDYQTLTNRT	ENQKLLAKQL	KNPDYVQKYA
Consensus	*****	*****	*****	*****	*****
	101		122		
msa20122.2{418_090}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_A909}	RAKYYFSKTG	EMIYPLPD--	--		
msa20122.2{418_1169NT}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_18RS21}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_2603}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_CJB110}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_COH1}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_H36B}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_JM9130013}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_M732}	RAKYYFSKTG	EMIYPLPD11	pk		
msa20122.2{418_M781}	RAKYYFSKTG	EMIYPLPD11	pk		
Consensus	*****	*****	--		

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8201
 STRAIN 2603
 ATGAAAATTTATTGGTTAAAATGTAAGGATAAGAAGTTAAAGCATTACACTTTTAGAA
 TGTTTGGTAGCATTGGTTACAATCACAGGAGCTTTACTAGTTTATCAAGGACTGACAAAA
 TTGTTGGCTCAACAGATAGTAGTGTCTTCTCCAGTCACTGATGGGTGTTATTA
 AcTCAGCAACTAAAATGCAGAATTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAAA
 CTTTATTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTC
 CGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAGACAATTGT
 CAAATGAGTCAGACCAAAAGTATGGTAAAACCTGTTTATTTTAAAGGACGGGTTAAAA
 AGGACATTTTACTATGATTTTAAAGAAGAACTTAA

SEQ ID NO. 8202
 STRAIN 090
 AATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTTA
 CGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTT
 CCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGT
 TAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTT
 TATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGAAGA
 AACT

SEQ ID NO. 8203
 STRAIN A909
 CAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTT
 TTTTATTTAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8204
 STRAIN H36B
 ATGCAGAAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTT
 TATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGA
 TGATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTT
 ATGGGTTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCT
 GTTTTATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAA
 AGAAGAACT

SEQ ID NO. 8205
 STRAIN 18RS21
 AGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTT
 TTTATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8206
 STRAIN M732
 CAGAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTAT
 TTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGA
 TTCCGTAAGACAGGTTATAAATGGTCGAGGTTATCAACCAATGGTTTATG
 GGTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTT
 TTTTATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGA
 AGAACT

SEQ ID NO. 8207
 STRAIN COHI
 GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACCTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TCCGTAAGACAGGTTATAAATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTT
 TTATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

SEQ ID NO. 8208
 STRAIN M781
 AGAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATT
 TACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TTCCGTAAGACAGGTTATAAATGGTCGAGGTTATCAACCAATGGTTTATGG
 GTTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTT
 TTTATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGAA
 GAACT

SEQ ID NO. 8209
 STRAIN CJB110
 GAATTCGAAGGCGCTCACTTGAATATTTAAGACAGAACAACTTTATTT
 ACCTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGAT
 TCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGG
 TTAGACAATTGTCAAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTT
 TTATTTTAAAGGACGGGTTAAAAGGACATTTTACTATGATTTTAAAGAAG
 AACT

Table 82: Comparative Sequences relating to SAG0165

SEQ ID NO. 8210

STRAIN 1169NT

TCCGAGGCGCTCACTTGGGAATATTTAAGACAGAACAACTTTATTACGT
AAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGATGATTTTCG
TAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTATGGGTTAG
ACAATTGTCAATGAGTCAAACCAAAAGTATGGTAAAACCTGTTTTTTAT
TTTTAAGGACGGTTAAAAAGGACATTTTACTATGATTTTAAAGAAGAAAC
T

SEQ ID NO. 8211

STRAIN JM9130013

TGCAGAATTTGAAGGCGCTCATCTGGAATATTTAAGACAGAACAACTTT
ATTTACGTAAGCAAGATAAGATTGTAACCTTTGGCAAATCTAATAAAGAT
GATTTCCGTAAGACAGGTTATGATGGTCGAGGTTATCAACCAATGGTTTA
TGGGTTAGACAATTTCAAATGAGTCAGACCAAAAGTATGGTAAAACCTTG
TTTTTTATTTTAAAGGACGGTTAAAAAGGACATTTTACTATGATTTTAAA
GAAGAACT

PRETTY of: /biotmp/msa128189.2{*} February 7, 2003 08:19 ..

msa128189.2{6_18RS21} 1 50
msa128189.2{6_2603} atgaaaaatt tattgttaaa atgtaaggat aagaaggta aagcatttac
msa128189.2{6_A909}
msa128189.2{6_H36B}
msa128189.2{6_JM9130013}
msa128189.2{6_COH1}
msa128189.2{6_M732}
msa128189.2{6_M781}
msa128189.2{6_090}
msa128189.2{6_CJB110}
msa128189.2{6_1169NT}
Consensus *****

msa128189.2{6_18RS21} 51 100
msa128189.2{6_2603} acttttagaa tgtttgtag cattggttac aatcacagga gctttactag
msa128189.2{6_A909}
msa128189.2{6_H36B}
msa128189.2{6_JM9130013}
msa128189.2{6_COH1}
msa128189.2{6_M732}
msa128189.2{6_M781}
msa128189.2{6_090}
msa128189.2{6_CJB110}
msa128189.2{6_1169NT}
Consensus *****

msa128189.2{6_18RS21} 101 150
msa128189.2{6_2603} tttatcaagg actgacaaaa ttggttgctc aacagatagt agtgaagtct
msa128189.2{6_A909}
msa128189.2{6_H36B}
msa128189.2{6_JM9130013}
msa128189.2{6_COH1}
msa128189.2{6_M732}
msa128189.2{6_M781}
msa128189.2{6_090}
msa128189.2{6_CJB110}
msa128189.2{6_1169NT}
Consensus *****

msa128189.2{6_18RS21} 151 200
msa128189.2{6_2603} tcttccagtc agtctgaatg ggtgttatta actcagcaac taaATGCaga
msa128189.2{6_A909}
msa128189.2{6_H36B}
msa128189.2{6_JM9130013}
msa128189.2{6_COH1}
msa128189.2{6_M732}
msa128189.2{6_M781}
msa128189.2{6_090}
msa128189.2{6_CJB110}
msa128189.2{6_1169NT}
Consensus *****

msa128189.2{6_18RS21} 201 250
msa128189.2{6_2603} atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTAC
msa128189.2{6_A909}
msa128189.2{6_H36B} atTtGAAGGC GCTCAtcTGG AATATTTAAG ACAGAACAAA CTTTATTAC

Table 82: Comparative Sequences relating to SAG0165

msa128189.2{6_JM9130013}	atTtGAAGGC	GCTCActGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_COH1}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_M732}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_M781}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_CJB110}	atTcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
msa128189.2{6_1169NT}	~TcGAAGGC	GCTCActTGG	AATATTTAAG	ACAGAACAAA	CTTTATTAC
Consensus	~*~*****	*****--***	*****	*****	*****
251					
msa128189.2{6_18RS21}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_2603}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_A909}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_H36B}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_JM9130013}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_COH1}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_M732}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_M781}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_090}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_CJB110}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTc
msa128189.2{6_1169NT}	GTAAGCAAGA	TAAGATTGTA	ACCTTTGGCA	AATCTAATAA	AGATGATTTt
Consensus	*****	*****	*****	*****	*****-
301					
msa128189.2{6_18RS21}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_2603}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_A909}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_H36B}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_JM9130013}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_COH1}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M732}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_M781}	CGTAAGACAG	GTTATaATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_090}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_CJB110}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
msa128189.2{6_1169NT}	CGTAAGACAG	GTTATgATGG	TCGAGGTTAT	CAACCAATGG	TTTATGGGTT
Consensus	*****	*****-***	*****	*****	*****
351					
msa128189.2{6_18RS21}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_2603}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_A909}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_H36B}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_JM9130013}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_COH1}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_M732}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_M781}	AGACAATTGT	CAAATGAGTC	AgACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_090}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_CJB110}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
msa128189.2{6_1169NT}	AGACAATTGT	CAAATGAGTC	AaACCAAAAG	TATGGTAAAA	CTTGTTTTTT
Consensus	*****	*****	*~*****	*****	*****
401					
msa128189.2{6_18RS21}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_2603}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_A909}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_H36B}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_JM9130013}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_COH1}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M732}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_M781}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_090}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_CJB110}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
msa128189.2{6_1169NT}	ATTTTAAGGA	CGGGTTAAAA	AGGACATTTT	ACTATGATTT	TAAAGAAGAA
Consensus	*****	*****	*****	*****	*****
451					
msa128189.2{6_18RS21}	ACT---				
msa128189.2{6_2603}	ACTtaa				
msa128189.2{6_A909}	ACT---				
msa128189.2{6_H36B}	ACT---				
msa128189.2{6_JM9130013}	ACT---				
msa128189.2{6_COH1}	ACT---				
msa128189.2{6_M732}	ACT---				
msa128189.2{6_M781}	ACT---				
msa128189.2{6_090}	ACT---				
msa128189.2{6_CJB110}	ACT---				
msa128189.2{6_1169NT}	ACT---				
Consensus	*****				

SEQ ID NO. 8212
 STRAIN 2603 frame: 1
 MNLLLLKCKDKKVKAFPTLLECLVALVTITGALLVYQGLTKLLAQQIVVMSSSSQSEWVLL
 TQQLNAEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTYDGRGYQPMVYGLDNC

Table 82: Comparative Sequences relating to SAG0165

QMSQTKSMVKLVFVFKDGLKRTFFYDFKEET.

SEQ ID NO. 8213
STRAIN 090 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKS
MVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8214
STRAIN A909 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8215
STRAIN H36B frame: 3
AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
KSMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8216
STRAIN 18RS21 frame: 2
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8217
STRAIN M732 frame: 3
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8218
STRAIN COH1 frame: 1
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8219
STRAIN M781 frame: 2
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYNGRGYQPMVYGLDNCQMSQTK
SMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8220
STRAIN CJB110 frame: 1
EFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
SMVKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8221
STRAIN 1169NT frame: 3
EFAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTKSM
VKLVFVFKDGLKRTFFYDFKEET

SEQ ID NO. 8222
STRAIN JM9130013 frame: 2
AEFEGAHLEYLRQNKLYLRKQDKIVTFGKSNKDDFRKTGYDGRGYQPMVYGLDNCQMSQTK
KSMVKLVFVFKDGLKRTFFYDFKEET

PRETTY of: /biotmp/msa128319.2{*} February 7, 2003 08:27 ..

1 50
msa128319.2{6_090}
msa128319.2{6_1169NT}
msa128319.2{6_18RS21}
msa128319.2{6_2603} mknlllkckd kkvkaftlle clvalvtitg allvyggtk llaqqivvms
msa128319.2{6_H36B}
msa128319.2{6_JM9130013}
msa128319.2{6_A909}
msa128319.2{6_CJB110}
msa128319.2{6_COH1}
msa128319.2{6_M732}
msa128319.2{6_M781}
Consensus *****

51 100
msa128319.2{6_090} -----fEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_1169NT} -----EG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_18RS21} -----EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_2603} sssqsewvll tqqlnAEfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_H36B} -----AEfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_JM9130013} -----AEfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_A909} -----EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_CJB110} -----EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_COH1} -----EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_M732} -----EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
msa128319.2{6_M781} -----EfEG AHLEYLRQNK LYLRKQDKIV TFGKSNKDDF
Consensus *****

Table 82: Comparative Sequences relating to SAG0165

	101	150
msa128319.2{6_090}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_1169NT}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_18RS21}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_2603}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_H36B}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_JM9130013}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_A909}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_CJB110}	RKTGYdGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_COH1}	RKTGYnGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_M732}	RKTGYnGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
msa128319.2{6_M781}	RKTGYnGRGY QPMVYGLDNC QMSQTKSMVK LVFYFKDGLK RTFYYDFKKE	
Consensus	*****-*****	*****
	151	
msa128319.2{6_090}	T-	
msa128319.2{6_1169NT}	T-	
msa128319.2{6_18RS21}	T-	
msa128319.2{6_2603}	T-	
msa128319.2{6_H36B}	T-	
msa128319.2{6_JM9130013}	T-	
msa128319.2{6_A909}	T-	
msa128319.2{6_CJB110}	T-	
msa128319.2{6_COH1}	T-	
msa128319.2{6_M732}	T-	
msa128319.2{6_M781}	T-	
Consensus	**	

Table 83: Comparative Sequences relating to SAG0108

SEQ ID NO. 8301

STRAIN 2603

atgaaaaagattcgcattatcaaaagtttattaaaatgattggttattttgtttttaaatt
agtgtagcagctagttttatttttccacgtgcccagttcgagatgataaatccttt
atttcaaatggtcaacgtaagcctggaaactctttatatgcttatgataaatcctttgat
aagctattaagcaaaaaatagaaaatgacaaacaaaataaaagcaagttgcttggat
gttccctgctgtaagaaaactcataagacagctgttgcggtcatggttttgcgaatagc
aaagagaatataagagccataggttggctgttccataagttaggatatacaatgcttctatg
cctgacaatattgcacatggtgaaagtcatgggcagttgataggctatggctggaacgac
cgcgagaacattatcaaatggacagaaatgatagttgataaagaatccatcaagccaaatt
actttatttgggtgttccaatgggtggagcaacagtcagatggctagtggtgaaaaatta
cctagtccaggtgttaatatcatggaagatgcccgttattctagtggttgggatgaatta
aaatttcaggctaaagagatgatggtttaccagcctcccactcttatatgaagttca
acaatttctaaaatcagagcaggttttccgtatggacaagcaagtagtgcgaaacaattg
aaaaagaataaattaccagccctcttattcatggtgataaggataaatttggttccaaca
agtatgggttatgacaaactataaagctacagcaggttaagaaagagctttatattgtaaaa
ggggcaaacatcggaatctttgaaacagagccagaaaaatagagaaacgtatctct
agttttttgaaaaaatatgaaaaa

SEQ ID NO. 8302

STRAIN 090

GCTAGTTTTATTTTTTCCACGTTGCCAAGTTCG
AGATGATAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCTTTGATAAGCTATTAAGCAAAAATAGAA
ATGACAACCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAA
GAAAACCTATAAGCAGCTGTTGTCGTTTCAATGGTTTGGCAATAGCAAAG
AGAAATAGAGGCATATGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCTGACATATGACATGGLGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCGGAGAACATTTATCAATGGACAGAAATGATAG
TTGATAAGAATCCATCAAGCCAATTACTTTaTTTGGTGTTCATGGGT
GGAGCAACAGTCATGATGGCTAGTGGTGA AAAATTAACCTAGTCAGGTTGT
TAATATCAATGAAAGATTGCGGTTATTCTAGTGTGGGATGAATTAATAA
TTCAGGCTAAAGAGATGATGGTTTACCAGCCTTCCCACTCTTATATGAA
GTTTCAACAATTTCAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
TAGTGTGCAACAATGAAAAAGAATAATTTACCAGCCCTCTTTATTCATG
GTGATAAGGATAAATTTGTTCCAAAGATATGGTTTATGACAACCTATAAAA
GCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAGGGGCAAAAACATGC
GAAATCTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
TTTTGAAAAATATGAAAAA

SEQ ID NO. 8303

STRAIN A909

AATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCT
TATGATAAATCCTTTGATAAGCTATTAAGCAAAAATAGAAATGACAAA
CCAAAATATAAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTC
ATAAGACAGCTGTTGTCGTTTCAATGGTTTGGCAATAGCAAAGAGAATATG
AAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTTATGCC
TGACAACATTGCACATGGTGAAGTCATGGGCAGTTGATAGGCTATGGCT
GGAACCGCCGGAACATTTCAAATGGACAGAAATGATAGTTGATAAG
AATTCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAAC
AGTCATGATGGCTAGTGGTGA AAAATTAACCTAGTCAGGTTGTTAATATCA
TTGAAGATGCGGTTTATCTGGTGTGGGATGAATTAATAATTCAGGCT
AAAGAGATGATGGTTTACCAGCCTTCCCACTCTTATATGAAAGTTTCAAC
AATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTAGTGTG
AACAATGAAAAAGAATAATTTACCAGCCCTTTTATTCATGGTGAATAAG
GATAAATTTGTTCCAACAAGTATGGTTTATGACAACCTATAAGCTACAGC
AGGTAAGAAAGAGCTTTATATTGTAAGGGGCAAAAACATGCGAAATCTT
TTGAAaCAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAA
AAATATGAAAAA

SEQ ID NO. 8304

STRAIN H36B

AGTTTTTATTTTTCCACGTTGCCAAGTTCGAGATGATAAATCCTTTAT
TTCAAATGGTCAACGTAAGCCTGGAAACTCTTTATATGCTTATGATAAAT
CCTTTGATAAGCTATTAAGCAAAAATAGAAATGACAAACCAAAATATA
AAGCAAGTTGCTTGGTATGTTCTGCTGCTAAGAAAACTATAAGACAGC
TGTTGTCGTTTATGGTTTGGCAATAGCAAAGAGAATATGAAGGCATATG
GTTGGCTGTTTCATAAGTTAGGATACAATGTTCTTTATGCTGACAACATT
GCACATGGTGAAGTCATGGGCAGTTGATAGGCTATGGCTGGAACGACCG
CGAGAACATTTCAAATGGACAGAAATGATAGTTGATAAGAAATTCATCAA
GCCAAATTACTTTATTTGGTGTTCATGGGTGGAGCAACAGTCATGATG
GCTAGTGGTGA AAAATTAACCTAGTCAGGTTGTTAATATCATTGAAGATTG
CGGTTATTTCTGGTGTGGGATGAATTAATAATTCAGGCTAAAGAGATGT
ATGGTTTACCAGCCTTCCCACTCTTATATGAAAGTTTCAACAATTTCTAAA
ATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTAGTGTGGAACAATTTGAA
AAAGAAATAATTTACCAGCCCTCTTTATTCATGGTGAATAAGGATAATTTG
TTCCAACAAGTATGGTTTATGACAACCTATAAGCTACAGCAGGTAAGAAA
GAGCTTTATATTGTAAGGGGCAAAAACATGCGAAATCTTTTGAACAGA
GCCAGAAAAATATGAGAAACGTATCTCTAGTTTTTTGAAAAATATGAAA
AA

SEQ ID NO. 8305

STRAIN 18RS21

Table 83: Comparative Sequences relating to SAG0108

GCTAGTTTTATTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAAA
 TGACAAACCAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGTTAAG
 AAAACTCATAAGACAGCTTGTGTCTGTTTTCATGGTTTTCGGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTT
 TTATGCTGACAACATATGCACATGGTGAAGTTCATGGGCAGTTGATAGGC
 TATGGCTGGAACCGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 TGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAATAATACCTAGTCAGGTTGTT
 AATATCATTGAAGATTTGGCTTATTCTAGTGTGGGATGAATAAAAAT
 TCAGGCTAAAGAGATGATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAaACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAA

SEQ ID NO. 8306
 STRAIN M732

GCTAGTTTTATTTTTCCACGTTGCCCAAGTTCGA
 GATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
 ATATGCTTATGATAAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAAA
 TGACAAACCAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTAAG
 AAAACTCATAAGACAGCTTGTGTCTGTTTTCATGGTTTTCGGAATAGCAAAGA
 GAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTT
 TTATGCTGACAACATATGCACATGGTGAAGTTCATGGGCAGTTGATAGGC
 TATGGCTGGAACCGACCGCGAGAACATTATCAAATGGACAGAAATGATAGT
 GGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GAGCAACAGTCATGATGGCTAGTGGTGAATAATACCTAGTCAGGTTGTT
 AATATCATTGAAGATTTGGCTTATTCTAGTGTGGGATGAATAAAAAT
 TCAGGCTAAAGAGATGATGGTTTACCAGCCTTCCCACTCTTATATGAAG
 TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
 AGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCATGG
 TGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAAAG
 CTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATGCG
 AAATCTTTTGAaACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTT
 TTTGAAAAAATATGAAAA

SEQ ID NO. 8307
 STRAIN COH1

GCTAGTTTTATTTTTCCACGTTGCCCAAGTTCC
 GAGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCT
 TTATATGCTTATGATAAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAA
 AATGAACAACCAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTA
 AGAAAACTCATAAGACAGCTTGTGTCTGTTTTCATGGTTTTCGGAATAGCAA
 GAAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 TCTTATGCTGACAACATATGCACATGGTGAAGTTCATGGGCAGTTGATAG
 GCTATGGCTGGAACCGACCGCGAGAACATTATCAAATGGACAGAAATGATA
 GTGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 TGGAGCAACAGTCATGATGGCTAGTGGTGAATAATACCTAGTCAGGTTG
 TTAATATCATTGAAGATTTGGCTTATTCTAGTGTGGGATGAATAAAAAT
 TTTGAGGCTAAAGAGATGATGGTTTACCAGCCTTCCCACTCTTATATGA
 AGTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAaACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAaaaaATATGAAAA

SEQ ID NO. 8308
 STRAIN M781

GCTAGTTTTATTTTTCCACGTTGCCCAAGTTCCG
 AGATGATAAAATCCTTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
 TATATGCTTATGATAAAATCCTTTGATAAGCTATTAAGCAAAAAATAGAA
 ATGACAAACCAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTAA
 GAAACTCATAAGACAGCTTGTGTCTGTTTTCATGGTTTTCGGAATAGCAAAG
 AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
 CTTATGCTGACAACATATGCACATGGTGAAGTTCATGGGCAGTTGATAGG
 CTATGGCTGGAACCGACCGCGAGAACATTATCAAATGGACAGAAATGATAG
 TGGATAAGAATCCATCAAGCCAAATTACTTTATTTGGTGTTCATGGGTG
 GGAGCAACAGTCATGATGGCTAGTGGTGAATAATACCTAGTCAGGTTGTT
 TAAATCATTGAAGATTTGGCTTATTCTAGTGTGGGATGAATAAAAAT
 TTCAGGCTAAAGAGATGATGGTTTACCAGCCTTCCCACTCTTATATGA
 GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAA
 GTAGTGTGCAACAATTGAAAAAGAATAATTTACCAGCCCTCTTTATTTCAT
 GGTGATAAGGATAAATTTGTTCCAACAAGTATGGTTTATGACAACTATAA
 AGCTACAGCAGGTAAGAAAGAGCTTTATATTGTAAAAGGGGCAAAACATG
 CGAAATCTTTTGAaACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGT
 TTTTGAaaaaATATGAAAA

SEQ ID NO. 8309

Table 83: Comparative Sequences relating to SAG0108

STRAIN CJB110
GCTAGTTTTTATTTTTCCACGTTGCCCAAGTTCGAG
ATGATAAATCCCTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTTA
TATGCTTATGATAAATCCCTTTGATAAGCTATTAAGCAAAAAATAGAAAT
GACAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTAAGA
AAACTCATAAGACAGCTGTTGTCGTTCAATGGTTTTGCGAATAGCAAAGAG
AATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
TATGCTGACAAATATGCACATGGTGAAAGTCATGGGCAGTTGATAGGCT
ATGGCTGGAACGACCCGAGAACATTATCAAATGGACAGAAATGATAGTT
GATAAGAATCCATCAAGCAAATTACTTTATTGGTGTTCATGGGTGG
AGCAAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTTA
ATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTA AAAATTT
CAGGCTAAAGAGATGATGTTTACCAGCCTTCCCACTCTTATATGAAGT
TTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGTA
gTGTGGAACAATGAAAAAGAAATAATTTACCAGCCCTcTTTATTcATGGT
GATAAGGATAAATTTGTTCCAACAAGTATGTTTATGACAACTATAAAGC
TACAGCAGGTAAGAAAGAGCTTTATATGTAAAAGGGGCAAAACATGCCA
AATCTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
TTGAAAAAATATGAAAA

SEQ ID NO. 8310

STRAIN 1169NT

GCTAGTTTTTATTTTTCCACGTTGCCCAAGTTCGA
GATGATAAATCCCTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTTT
ATATGCTTATGATAAATCCCTTTGATAAGCTATTAAGCAAAAAATAGAAA
TGACAAACCcAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGCTAAG
AAAACTCATAAGACAGCTGTTGTCGTTCAATGGTTTTGCGAATAGCAAAGA
gAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTTcT
TTATACCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
TATGGCTGGAACGACCCGAGAACATTATCAAATGGACAGAAATGATAGT
TGATAAGAATCCATCAAGCAAATTACTTTATTGGTGTTCATGGGTGG
GAGCAAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGTT
AATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTA AAAATTT
TCAGGCTAaAGAGATGATGTTTACCAGCCTTCCCACTcTTATATGAAG
TTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAGT
AGTGTAGAACAAATGAAAAAGAAATAATTTACCAGCCCTCTTTATTcATGG
TGATAAGGATAAATTTGTTCCAACAAGTATGTTTATGACAACTATAAAG
CTACAGCAGGTAAGAAAGAGCTTTATATGTAAAAGGGGCAAAACATGCC
AAATCTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTTTT
TTTAAAAAATATGAAAA

SEQ ID NO. 8311

STRAIN JM9130013

GCTAGTTTTTATTTTTCCACGTTGCCCAAGTTCG
AGATGATAAATCCCTTATTTCAAATGGTCAACGTAAGCCTGGAAACTCTT
TATATGCTTATGATAAATCCCTTTGATAAGCTATTAAGCAAAAAATAGAA
ATGAcAAACCAAAATATAAAGCAAGTTGCTTGGTATGTTCCCTGCTGTTAA
GAAAACTCATAAGACAGCTGTTGTCGTTCAATGGTTTTGCGAATAGCAAAG
AGAATATGAAGGCATATGGTTGGCTGTTTCATAAGTTAGGATACAATGTT
CTTATGCTGACAAATATTGCACATGGTGAAAGTCATGGGCAGTTGATAGG
CTATGGCTGGAACGACCCGAGAACATTATCaAATGGACAGAAATGATAG
TTGATAAGAATCCATCAAGCAAATTACTTTATTGGTGTTCATGGGTGG
GGCAAACAGTCATGATGGCTAGTGGTGAAAAATTACCTAGTCAGGTTGT
TAATATCATTGAAGATTGCGGTTATTcTAGTGTTTGGGATgAATTA AAAATTT
TTCAAGCTAAAGAGATGATGTTTACCAGCCTTCCCACTCTTATATGAAG
GTTTCAACAATTTCTAAAATCAGAGCAGGTTTTTCGTATGGACAAGCAAG
TAGTGTGGAACAATGAAAAAGAAATAATTTACCAGCCCTCTTTATTcATG
GTGATAAGGATAAATTTGTTCCAACAAGTATGTTTATGACAACTATAAAG
GCTACAGCAGGTAAGAAAGAGCTTTATATGTAAAAGGGGCAAAACATGCC
GAAATCTTTGAAACAGAGCCAGAAAAATATGAGAAACGTATCTCTAGTT
TTTAAAAAATATGAAAA

PRETTY of: /biotmp/msa286608.2{*} February 24, 2003 06:26 ..

Table with sequence alignment. Columns include sequence identifiers (e.g., msa286608.2{662_COH1}), alignment positions (1, 51, 100), and sequence characters. Consensus sequence is shown at the bottom.

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_A909}	-----	-----	-----	-----	-----
msa286608.2{662_H36B}	-----	-----	--agtttttta	ttttttccac	gttgcccaag
msa286608.2{662_090}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_CJB110}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_18RS21}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_2603}	gtttttaatt	agtgttagcag	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_JM9130013}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
msa286608.2{662_1169NT}	-----	-----	ctagtttttta	ttttttccac	gttgcccaag
Consensus	*****	*****	-----	-----	-----

101						150					
msa286608.2{662_COH1}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_M732}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_M781}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_A909}	-----	--AATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_H36B}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_090}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_CJB110}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_18RS21}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_2603}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_JM9130013}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
msa286608.2{662_1169NT}	ttcgagatga	taAATCCTTT	ATTTCAAATG	GTCAACGTAA	GCCTGGAAAC						
Consensus	-----	*****	*****	*****	*****						

151						200					
msa286608.2{662_COH1}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_M732}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_M781}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_A909}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_H36B}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_090}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_CJB110}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_18RS21}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_2603}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_JM9130013}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
msa286608.2{662_1169NT}	TCTTTATATG	CTTATGATAA	ATCCTTTGAT	AAGCTATTAA	AGCAAAAAAT						
Consensus	*****	*****	*****	*****	*****						

201						250					
msa286608.2{662_COH1}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_M732}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_M781}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_A909}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_H36B}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_090}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_CJB110}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_18RS21}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_2603}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_JM9130013}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
msa286608.2{662_1169NT}	AGAAATGACA	AACCAAATA	TAAAGCAAGT	TGCTTGGTAT	GTTCCCTGCTG						
Consensus	*****	*****	*****	*****	*****						

251						300					
msa286608.2{662_COH1}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_M732}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_M781}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_A909}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_H36B}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_090}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_CJB110}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_18RS21}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_2603}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_JM9130013}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
msa286608.2{662_1169NT}	cTAAGAAAAC	TCATAAGACA	GcTGTGTGTCG	TTCATGGTTT	TGCGAATAGC						
Consensus	*****	*****	*_*_*_*_*_*_*_*	*****	*****						

301						350					
msa286608.2{662_COH1}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_M732}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_M781}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_A909}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_H36B}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_090}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_CJB110}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_18RS21}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_2603}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_JM9130013}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
msa286608.2{662_1169NT}	AAAGAGAATA	TGAAGGCATA	TGGTTGGCTG	TTTCATAAGT	TAGGATACAA						
Consensus	*****	*****	*****	*****	*****						

351						400					
msa286608.2{662_COH1}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA						
msa286608.2{662_M732}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA						

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M781}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_A909}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_H36B}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_090}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_CJB110}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_18RS21}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_2603}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_JM9130013}	TGTTCTTATg	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
msa286608.2{662_1169NT}	TGTTCTTATa	CCTGACAAcA	TTGCACATGG	TGAAAGTCAT	GGGCAGTTGA
Consensus	*****-*	*****-*	*****	*****	*****
	401				450
msa286608.2{662_COH1}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M732}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_M781}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_A909}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_H36B}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_090}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_CJB110}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_18RS21}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_2603}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_JM9130013}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
msa286608.2{662_1169NT}	TAGGCTATGG	CTGGAACGAC	CGCGAGAACA	TTATCAAATG	GACAGAAATG
Consensus	*****	*****	*****	*****	*****
	451				500
msa286608.2{662_COH1}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_M732}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_M781}	ATAGTgGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_A909}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_H36B}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_090}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_CJB110}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_18RS21}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_2603}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_JM9130013}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
msa286608.2{662_1169NT}	ATAGTtGATA	AGAATcCATC	AAGCCAAATT	ACTTTATTgG	GTGTTTCAAT
Consensus	****-****	****-****	*****	*****	*****
	501				550
msa286608.2{662_COH1}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M732}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_M781}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_A909}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_H36B}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_090}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_CJB110}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_18RS21}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_2603}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_JM9130013}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
msa286608.2{662_1169NT}	GGGTGGAGCA	ACAGTCATGA	TGGCTAGTGG	TGAAAAATTA	CCTAGTCAGG
Consensus	*****	*****	*****	*****	*****
	551				600
msa286608.2{662_COH1}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M732}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_M781}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_A909}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_H36B}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTgGTGTTTg	GGATGAATTA
msa286608.2{662_090}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_CJB110}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_18RS21}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_2603}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_JM9130013}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
msa286608.2{662_1169NT}	TTGTTAATAT	CATTGAAGAT	TGcGGTTATT	CTaGTGTTTg	GGATGAATTA
Consensus	*****	*****	**-*****	**-*****	*****
	601				650
msa286608.2{662_COH1}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_M732}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_M781}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_A909}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_H36B}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_090}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_CJB110}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_18RS21}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_2603}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_JM9130013}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
msa286608.2{662_1169NT}	AAATTCAGG	CTAAAGAGAT	GTATGGTTTA	CCAGCCTTCC	CACTCTTATA
Consensus	*****	*****	*****	*****	*****
	651				700
msa286608.2{662_COH1}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG

Table 83: Comparative Sequences relating to SAG0108

msa286608.2{662_M732}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_M781}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_A909}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_H36B}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_090}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_CJB110}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_18RS21}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_2603}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_JM9130013}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
msa286608.2{662_1169NT}	TGAAGTTTCA	ACAATTTCTA	AAATCAGAGC	AGGTTTTTTCG	TATGGACAAG
Consensus	*****	*****	*****	*****	*****

msa286608.2{662_COH1}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_M732}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_M781}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_A909}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_H36B}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_090}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_CJB110}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_18RS21}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_2603}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_JM9130013}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
msa286608.2{662_1169NT}	CAAGTAGTGT	cGAACAATTG	AAAAAGAATA	ATTTACCAGC	CCTCTTTTATT
Consensus	*****	*****	*****	*****	*****

msa286608.2{662_COH1}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M732}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_M781}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_A909}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_H36B}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_090}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_CJB110}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_18RS21}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_2603}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_JM9130013}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
msa286608.2{662_1169NT}	CATGGTGATA	AGGATAATTT	TGTTCCAACA	AGTATGGTTT	ATGACAACCTA
Consensus	*****	*****	*****	*****	*****

msa286608.2{662_COH1}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M732}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_M781}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_A909}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_H36B}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_090}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_CJB110}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_18RS21}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_2603}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_JM9130013}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
msa286608.2{662_1169NT}	TAAAGCTACA	GCAGGTAAGA	AAGAGCTTTA	TATTGTAAAA	GGGGCAAAAC
Consensus	*****	*****	*****	*****	*****

msa286608.2{662_COH1}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M732}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_M781}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_A909}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_H36B}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_090}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_CJB110}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_18RS21}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_2603}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_JM9130013}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
msa286608.2{662_1169NT}	ATGCCGAAATC	TTTTGAAACA	GAGCCAGAAA	AATATGAGAA	ACGTATCTCT
Consensus	*****	*****	*****	*****	*****

msa286608.2{662_COH1}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M732}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_M781}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_A909}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_H36B}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_090}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_CJB110}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_18RS21}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_2603}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_JM9130013}	AGTTTTTTGA	AAAAATATGA	AAAA		
msa286608.2{662_1169NT}	AGTTTTTTGA	AAAAATATGA	AAAA		
Consensus	*****	*****	****		

Table 83: Comparative Sequences relating to SAG0108

STRAIN 2603 frame: 1
 MKKIRLSKFIKMIIVVLLFLISVAASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFD
 KLLKQKIEMTNQNIKQVAWYVPAVKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLM
 PDNIAHGESHGQLIGYGWNDRENI IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKL
 PSQVUNI IEDCGYSSVWDELKFKQAKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQL
 KKNLPALEFIHGDKDNFVPTSMVYDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRIS
 SFLKKEYK

SEQ ID NO. 8313
STRAIN 090 frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8314
STRAIN A909 frame: 3
 SFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPAKTKHTAVVVHGFAN
 SKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENI IKWTEMI VDKNSSS
 QITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQAKEMYGLPAFPPLLYE
 VSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMVYDNYKATAGKKELYI
 VKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8315
STRAIN H36B frame: 1
 SFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 KTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDRENI
 IKWTEMI VDKNSSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8316
STRAIN I8RS21 frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 VKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8317
STRAIN M732 frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8318
STRAIN COH1 frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8319
STRAIN M781 frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8320
STRAIN CJB110 frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLMPDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8321
STRAIN I169NT frame: 1
 ASFYFFHVAQVRDDKSFISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
 AKKTKHTAVVVHGFANSKENMKAYGWLPHKLGYNVLI PDNIAHGESHGQLIGYGWNDREN
 I IKWTEMI VDKNPSSQITLFGVSMGGATVMMASGEKLPSQVUNI IEDCGYSSVWDELKFKQ
 AKEMYGLPAFPPLLYEVSTISKIRAGFSYQGASSVEQLKKNLPALEFIHGDKDNFVPTSMV
 YDNYKATAGKKELYIVKGAKHAKSFETEPEKYEKRISFLKKEYK

SEQ ID NO. 8322

Table 83: Comparative Sequences relating to SAG0108

STRAIN JM9130013 frame: 1

ASFYFFHVAQVRDDKSF ISNGQRKPGNSLYAYDKSFDKLLKQKIEMTNQNIKQVAWYVPA
VKKTHKTAVVVHGFANSKENMKAYGWL FHKLGYNVLM PDNIAHGESHGQLIGYGWNDREN
I IKWTEMI VDKNPSQI TLFVSMGGA TVMMASGEKLP SQVVNI I EDCGYSVWDELKFPQ
AKEMYGL PAFPLLYEVS TISKIRAGFS YQASSVEQL KKNL PALFI HGDKNFVPTSMV
YDNYKATAGKELYIVK GAKHAKSFET EPEKYEKRISSFLKKEYK

PRETTY of: /biotmp/msa286876.2{*} February 24, 2003 06:46 ..

Table with 2 columns: sequence identifiers (e.g., msa286876.2{662_A909}) and sequence alignments. Includes a Consensus line at the bottom.

Table with 2 columns: sequence identifiers (e.g., msa286876.2{662_A909}) and sequence alignments. Includes a Consensus line at the bottom.

Table with 2 columns: sequence identifiers (e.g., msa286876.2{662_A909}) and sequence alignments. Includes a Consensus line at the bottom.

Table with 2 columns: sequence identifiers (e.g., msa286876.2{662_A909}) and sequence alignments. Includes a Consensus line at the bottom.

Table with 2 columns: sequence identifiers (e.g., msa286876.2{662_A909}) and sequence alignments. Includes a Consensus line at the bottom.

Table with 2 columns: sequence identifiers (e.g., msa286876.2{662_A909}) and sequence alignments. Includes a Consensus line at the bottom.

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8401
 STRAIN 2603
 ATGATGAAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACTAAAC
 AATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATCATAGCATTAAATTTG
 ATGCCAGCCATTGATTTTAAATGCAATCAATTGATTTAGAACCCTCAAGATTGGACCGT
 ATCGTAGTAGCAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGTACAGCA
 AAAATGCTAGCTTATACGCTTAAGATTGACTTAGTGGAGTATCTAGCCTGTACGCTTTA
 ACAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATGCACGACGTAATAAT
 GTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACTGTACACTTCTCTT
 GAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAATGTTTCATTTTGTCCGAGAGGTTGCA
 GCATTTTGTGATCAGATTAAGAAAGCCTTACCACATGCTAAAATACAGAAAACCTTACCT
 TGTGCAGTAGCAATGGGGCGCAAAGGACAAAATGAAAAGCGTTAATGTAGATGCGTTT
 GTTCCACGATACTTAAAACGTTGTTGAAGCTGAGGAAAATGGTTAAAAAACCACTGTGAA
 ACGAATACAGAAGAAATATATTAAGAGAGTT

SEQ ID NO. 8402
 STRAIN 090
 AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAGTGGCTGTACT
 AAACAATATGGAATGTTTAGCGACTGTCACTATCAATATCAAAAAGAAATC
 ATAGCATTAATTTGATGCCAGCCATTGATTTTAAATGCAATCAATTGAT
 TTAGAACCCTCAAGATTGGACCGTATCGTAGTGGCAGAGGGTCCAGGATC
 TTATACGGGCTTACGTGTAGCTGTTGTACAGCAAAAATGCTAGCTTATA
 CGCTTAAGATTGACTTAGTGGAGTATCTAGCCTGTACGCTTTAACAAAT
 GGATTTTCAGAAAATGATTTGTTGGTACCCTTATAGATGCACGACGTA
 CAATGTTTATGTTGGTTTCTATCAAAATGGTGATACTGTTAAACCAGACT
 GTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGAATAAAGCCAAT
 GTTCATTTGTGCGAGAGGTTGCAGCATTTTGTGATCAGATTAAgAAAGC
 CTTACCACATGCTAAAATTAAGAAAACCTTACCTTGTGCAGTGGCAATTTG
 GCGCAAAGGACAAAATGGAAGCGTTAATGTAGATGCGTTTGTGCA
 CGATACTTAAAACGAGTTGAAGCTGAGGAAAATGGTTAAAAAACCACTG
 TGAACGAAT

SEQ ID NO. 8403
 STRAIN A909
 AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCAG
 TGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATATC
 AAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCA
 ATCAATTTGATTTAGAACCCTCAAGATTGGACCGTATCGTAGTAGCAGAGG
 GTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAATG
 CTAGCTTATACGCTTAAGATTGACTTAGTGGAGTATCTAGCCTGTACGC
 TTTAACAAAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGATG
 CACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGTT
 AAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 TAAAGCCAATGTTTCATTTTGTCCGAGAGGTTGCAGCATTTGTTGACCAGA
 TTAAGAAAGTTTACCACATGCTAAAATTAAGAAAACCTTACCTTGTGCA
 GCGCAATTTGGGCGCAAAGGACAAAATGAAAAGCGTTAATGTAGATGC
 GTTTGTTCCACGATACTTAAAACGTTGTTGAAGCTGAGGAAAATGGTTAA
 GAAACCACTGTGAAACGAAT

SEQ ID NO. 8404
 STRAIN H36B
 AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCA
 AATCAATTTGATTTAGAACCCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTGGAGTATCTAGCCTGTACG
 CTTTAAACAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTCCGAGAGGTTGCAGCATTTGTTGACCAG
 ATTAAGAAAGTTTACCACATGCTAAAATTAAGAAAACCTTACCTTGTGCA
 AGTGGCAATTTGGGCGCAAAGGACAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTCCACGATACTTAAAACGTTGTTGAAGCTGAGGAAAATGGTTAA
 AGAAACCACTGTGAAACGAATACAGAAGAAATATATTAAGAGAGTT

SEQ ID NO. 8405
 STRAIN 18RS21
 AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
 GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCACTATCAATAT
 CAAAAAGAAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTAAATGCA
 AATCAATTTGATTTAGAACCCTCAAGATTGGACCGTATCGTAGTAGCAGAG
 GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
 GCTAGCTTATACGCTTAAGATTGACTTAGTGGAGTATCTAGCCTGTACG
 CTTTAAACAATGGATTTTCAGAAAATGATTTATTTGGTACCCTTATAGAT
 GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAAATGGAGATACTGT
 TAAACCAGACTGTCACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
 ATAAAGCCAATGTTTCATTTTGTCCGAGAGGTTGCAGCATTTTGTGATCAG
 ATTAAGAAAGCCTTACCACATGCTAAAATTAAGAAAACCTTACCTTGTGCA
 AGTAGCAATTTGGGCGCAAAGGACAAAATGAAAAGCGTTAATGTAGATG
 CGTTTGTCCACGATACTTAAAACGTTGTTGAAGCTGAGGAAAATGGTTAA
 AAAAAACCACTGTGAAACGAATACAGAAGAAATATATTAAGAGAGTT

Table 84: Comparative Sequences relating to SAG0267

SEQ ID NO. 8406

STRAIN M732

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTAaCTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATGGTACCACCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCAATTTTGTGGAGAGGTTGCAGCATTTTTTGATCAG
ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGAnn
CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCCTGTGAAACGAATACAGAAGAAATATATTAAGAGAGTT

SEQ ID NO. 8407

STRAIN COHI

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCAC
TATCAGTGGCTGTAaCTAAACAATATGGAATGTTTAGCGACTGTCACATC
AATATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTT
AATCAAACTCAATTTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAG
CAGAGGGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCA
AAAAATGCTAGCTTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCT
GTACGCTTTAACAAATGGATTTTCAGAAAATGATTTATGGTACCACCTTA
TAGATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAATGGTGAT
ACTGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGT
GGGGAATAAAGCCAATGTTCAATTTTGTGGAGAGGTTGCAGCATTTTTTG
ATCAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCT
TGTGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGT
AGATGCGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATT
GTTAAAAAACCACTGTGAAACGAATACAGAAGAAATATATTAAGAGAGTT

SEQ ID NO. 8408

STRAIN M781

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTA
TCAGTGGCTGTAaCTAAACAATATGGAATGTTTAGCGACTGTCACATCAA
TATCAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAA
TGCAATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTATCA
GAGGTTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAA
AATGCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGT
ACGCTTTAACAAATGGATTTTCAGAAAATGATTTATGGTACCACCTTATA
GATGCACGACGTAACAATGTTTATGTTGGTTTCTATCAAATGGTGATACT
TGTTAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGG
GGAATAAAGCCAATGTTCAATTTTGTGGAGAGGTTGCAGCATTTTTTGAT
CAGATTAAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTG
TGCAGTAGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAG
ATGCGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGG
TTAAAAAACCACTGTGAAACGAATACAGAAGAAATATATTAAGAGAGTT

SEQ ID NO. 8409

STRAIN CJB110

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTAaCTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTGTTGGTACCACCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCAATTTTGTGGAGAGGTTGCAGCATTTTTTGATCAG
ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGAAAAGCGTTAATGTAGATG
CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AAAAACCCTGTGAAACGAATACAGAAGAAATATATTAAGAGAGTT

SEQ ID NO. 8410

STRAIN I169NT

AAAGTTTGTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTAaCTAAACAATATGGAATGTTTAGCGACTGTCACATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAAATGC
AATCAATTGATTTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
GCTAGCTTATACGCTTAAGATTGACTTAGTTGGAGTATCTAGCCTGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATGGTACCACCTTATAGAT
GCACGACGTAACAATGTTTATGTTGGTTTCTATCAAATGGTGATACTGT
TAAACCAGACTGTCACACTTCTCTTGAAGAAGTCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCAATTTTGTGGAGAGGTTGCAGCATTTTTTGATCAG
ATTAAGAAAGCCTTACCACATGCTAAAATTACAGAAACTTTACCTTGTGC

Table 84: Comparative Sequences relating to SAG0267

AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAgATG
CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAgGAAAATTGGTTA
AAAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

SEQ ID NO.: 8411
STRAIN JM9130013

AAAGTTTTAGCCTTTGATACTTCAAGCAAAGCACTATCA
GTGGCTGTACTAAACAATATGGAATGTTTAGCGACTGTCATCAATAT
CAAAAAGAATCATAGCATTAAATTTGATGCCAGCCATTGATTTTTTAATGC
AATCAATTGATTAGAACCTCAAGATTTGGACCGTATCGTAGTAGCAGAG
GGTCCAGGATCTTATACGGGCTTACGTGTAGCTGTTGCTACAGCAAAAAT
gCTAGCTTATACGCTTAAAGATTGACTTAGTTGGAGTATCTAGCCGTACG
CTTTAACAAATGGATTTTCAGAAAATGATTTATTGGTACCCTTATAGAT
GCACGACGTAACAATGTTATGTTGGTTTCTATCAAAATGGAGATACTGT
TAAACCAAGCTGTCACTTCTCTTGAAGAAGCTTACAAGAGGTGGGGA
ATAAAGCCAATGTTCAATTTGTTCGAGAGGTTGCAGCATTGTTGTACCAG
ATTAAGAAAGTTTACCACATGCTAAAATTACAGAACTTTACCTTGTGC
AGTGGCAATTGGGCGCAAAGGACAAAAATGGAAGCGTTAATGTAgATG
CGTTTGTTCACGATACTTAAAACGTGTTGAAGCTGAGGAAAATTGGTTA
AGAAACCACTGTGAAACGAATACAGAAGAATATATTAAGAGAGTT

PRETTY of: /biotmp/msa521675.2{*} March 10, 2003 08:34 ..

msa521675.2{69_A909} 1 50
msa521675.2{69_H36B} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_JM9130013} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_1169NT} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_090} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_CJB110} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_18RS21} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_2603} atgatgAAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_COH1} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M732} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
msa521675.2{69_M781} -----AAAG TTTTAGCCCTT TGATACTTCA AGCAAAGCAC TATCAGTGGC
Consensus *****

msa521675.2{69_A909} 51 100
msa521675.2{69_H36B} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_JM9130013} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_1169NT} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_090} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_CJB110} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_18RS21} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_2603} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_COH1} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_M732} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
msa521675.2{69_M781} TGTACTAAAC AATATGGAAT GTTTAGCGAC TGTCACTATC AATATCAAAA
Consensus *****

msa521675.2{69_A909} 101 150
msa521675.2{69_H36B} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_JM9130013} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_1169NT} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_090} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_CJB110} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_18RS21} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_2603} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_COH1} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M732} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
msa521675.2{69_M781} AGAATCATAG CATTAATTG ATGCCAGCCA TTGATTTTTT AATGCAATCA
Consensus *****

msa521675.2{69_A909} 151 200
msa521675.2{69_H36B} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_JM9130013} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_1169NT} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_090} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_CJB110} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTgg CAGAGGGTCC
msa521675.2{69_18RS21} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_2603} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_COH1} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_M732} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTAg CAGAGGGTCC
msa521675.2{69_M781} ATTGATTAG AACCTCAAGA TTTGGACCGT ATCGTAGTat CAGAGGGTCC
Consensus *****

msa521675.2{69_A909} 201 250
msa521675.2{69_H36B} AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG
AGGATCTTAT ACGGGCTTAC GTGTAGCTGT TGCTACAGCA AAAATGCTAG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_JM9130013}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_1169NT}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_090}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_CJB110}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_18RS21}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_2603}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_COH1}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_M732}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
msa521675.2{69_M781}	AGGATCTTAT	ACGGGCTTAC	GTGTAGCTGT	TGCTACAGCA	AAAATGCTAG
Consensus	*****	*****	*****	*****	*****

	251				300
msa521675.2{69_A909}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_H36B}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_JM9130013}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_1169NT}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_090}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_CJB110}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_18RS21}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_2603}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_COH1}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M732}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
msa521675.2{69_M781}	CTTATACGCT	TAAGATTGAC	TTAGTTGGAG	TATCTAGCCT	GTACGCTTTA
Consensus	*****	*****	*****	*****	*****

	301				350
msa521675.2{69_A909}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_H36B}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_JM9130013}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_1169NT}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_090}	ACAAATGGAT	TTTCAGAAAA	TGATTTgTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_CJB110}	ACAAATGGAT	TTTCAGAAAA	TGATTTgTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_18RS21}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_2603}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_COH1}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M732}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
msa521675.2{69_M781}	ACAAATGGAT	TTTCAGAAAA	TGATTTaTTG	GTACCACITTA	TAGATGCACG
Consensus	*****	*****	*****-***	*****	*****

	351				400
msa521675.2{69_A909}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_H36B}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_JM9130013}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGaGAT	ACTGTTAAAC
msa521675.2{69_1169NT}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_090}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_CJB110}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_18RS21}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_2603}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_COH1}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M732}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
msa521675.2{69_M781}	ACGTAAcAAT	GTTTATGTTG	GTTTCTATCA	AAATGGtGAT	ACTGTTAAAC
Consensus	*****-***	*****	*****	*****-***	*****

	401				450
msa521675.2{69_A909}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_H36B}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_JM9130013}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_1169NT}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_090}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_CJB110}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_18RS21}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_2603}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_COH1}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M732}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
msa521675.2{69_M781}	CAGACTGTCA	CACCTTCTCT	GAAGAAGTCT	TACAAGAGGT	GGGGAATAAA
Consensus	*****	*****	*****	*****	*****

	451				500
msa521675.2{69_A909}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_H36B}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_JM9130013}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTgTTG	AcCAGATTAA
msa521675.2{69_1169NT}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_090}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_CJB110}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_18RS21}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_2603}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_COH1}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_M732}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
msa521675.2{69_M781}	GCCAAATGTTc	ATTTTGTcCGG	AGAGGTTGCA	GCATTTtTTG	AcCAGATTAA
Consensus	*****	*****	*****	*****-***	*-*****

	501				550
msa521675.2{69_A909}	GAAAGtTTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG

Table 84: Comparative Sequences relating to SAG0267

msa521675.2{69_H36B}	GAAAGctTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_JM9130013}	GAAAGctTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_1169NT}	GAAAGctTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_090}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_CJB110}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_18RS21}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_2603}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_COH1}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M732}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
msa521675.2{69_M781}	GAAAGccTTA	CCACATGCTA	AAATTACAGA	AACTTTACCT	TGTGCAGTgG
Consensus	*****-***	*****	*****	*****	*****
551					
msa521675.2{69_A909}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_H36B}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_JM9130013}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_1169NT}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_090}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_CJB110}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_18RS21}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_2603}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_COH1}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
msa521675.2{69_M732}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAnnCGTTT
msa521675.2{69_M781}	CAATTGGGCG	CAAAGGACAA	AAAATGaaaa	CGGTTAATGT	AGAtgCGTTT
Consensus	*****	*****	*****-***	*****	***-*****
601					
msa521675.2{69_A909}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_H36B}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_JM9130013}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAgAAA
msa521675.2{69_1169NT}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_090}	GTTCCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_CJB110}	GTTCCACGAT	ACTTAAAACG	aGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_18RS21}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_2603}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_COH1}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M732}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
msa521675.2{69_M781}	GTTCCACGAT	ACTTAAAACG	tGTTGAAGCT	GAGGAAAATT	GGTTAAaAAA
Consensus	*****	*****	-*****	*****	*****-***
616					
msa521675.2{69_A909}	CCACTGTGAA	ACGAAT----	-----	-----	-----
msa521675.2{69_H36B}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_JM9130013}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_1169NT}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_090}	CCACTGTGAA	ACGAAT----	-----	-----	-----
msa521675.2{69_CJB110}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_18RS21}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_2603}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_COH1}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_M732}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
msa521675.2{69_M781}	CCACTGTGAA	ACGAATACAG	AAGAATATAT	TAAGAGAGTT	-----
Consensus	*****	*****	*****	*****	*****

SEQ ID NO. 8412
 STRAIN 2603 frame: 1
 MKVLAFDTSSKALSVAVLNNMECLATVTINI KKNHSINLMPAIDFLMQSIDLEPQDLDR
 IVVAEGPGSYTGLRVAVATAKMLAYTLKI DLVGVSSLYALTNGFSENDLLVPLIDARRNN
 VYVGFYQNGDITVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKALPHAKITETLPCA
 CAVAIGRKGQKMKSVNVDVAFVPRYLKRVAEABENWLNKHCETNTTEEYIKRV

SEQ ID NO. 8413
 STRAIN 090 frame: 1
 KVLAFDTSKALSVAVLNNMECLATVTINI KKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKI DLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDITVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDVAFVPRYLKRVAEABENWLNKHCETN

SEQ ID NO. 8414
 STRAIN A909 frame: 1
 KVLAFDTSKALSVAVLNNMECLATVTINI KKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKI DLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDITVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDVAFVPRYLKRVAEABENWLNKHCETN

SEQ ID NO. 8415
 STRAIN H36B frame: 1
 KVLAFDTSKALSVAVLNNMECLATVTINI KKNHSINLMPAIDFLMQSIDLEPQDLDRIV
 VAEGPGSYTGLRVAVATAKMLAYTLKI DLVGVSSLYALTNGFSENDLLVPLIDARRNNVY
 VGFYQNGDITVKPDCHTSLEEVLQEVGNKANVHFVGEVAAFVDQIKKALPHAKITETLPCA
 VAIGRKGQKMKSVNVDVAFVPRYLKRVAEABENWLNKHCETNTTEEYIKRV

SEQ ID NO. 8416

Table 84: Comparative Sequences relating to SAG0267

STRAIN 18RS21 frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

SEQ ID NO. 8417
STRAIN M732 frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVXXFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

SEQ ID NO. 8418
STRAIN COH1 frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

SEQ ID NO. 8419
STRAIN M781 frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VSEGPSTYGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

SEQ ID NO. 8420
STRAIN CJB110 frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

SEQ ID NO. 8421
STRAIN I169NT frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

SEQ ID NO. 8422
STRAIN JM9130013 frame: 1
KVLAFDTSKALSVAVLNNMECLATVTINIKKNHSINLMPAIDFLMQSIDLEPQDLDRIV
VAEGPGSYTGLRVAVATAKMLAYTLKIDLGVVSSLYALTNGFSENDLLVPLIDARRNNVY
VGFYQNGDVTVPKDCHTSLEEVLQEVGNKANVHFVGEVAFFDQIKKALPHAKITETLP
CAVAIGRKGQKMKSVNVDAFVPRYLKRVABEENWLNKHCETNTEBEYIKRV

PRETTY of: /biotmp/msa521982.2{*} March 10, 2003 08:40 ..

msa521982.2{69_A909} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS 50
msa521982.2{69_H36B} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_JM9130013} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_090} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_CJB110} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_18RS21} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_2603} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_COH1} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M781} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_I169NT} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
msa521982.2{69_M732} --KVLAFDTS SKALSVAVLN NMECLATVTI NIKKNHSINL MPAIDFLMQS
Consensus *****

msa521982.2{69_A909} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL 100
msa521982.2{69_H36B} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_JM9130013} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_090} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_CJB110} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_18RS21} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_2603} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_COH1} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M781} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_I169NT} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
msa521982.2{69_M732} IDLEPQDLDR IVVaEGPGSY TGLRVAVATA KMLAYTLKID LVGVSSLYAL
Consensus *****

msa521982.2{69_A909} TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPCDCHTSL EEVLQEVGNK 150
msa521982.2{69_H36B} TNGFSENDLL VPLIDARRNN VYVGFYQNGD TVKPCDCHTSL EEVLQEVGNK

Table 84: Comparative Sequences relating to SAG0267

msa521982.2{69_JM9130013}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_090}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_CJB110}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_18RS21}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_2603}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_COH1}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M781}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_1169NT}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
msa521982.2{69_M732}	TNGFSENDLL	VPLIDARRNN	VYVGFYQNGD	TVKPDCHTSL	EEVLQEVGNK
Consensus	*****	*****	*****	*****	*****
151					
msa521982.2{69_A909}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_H36B}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_JM9130013}	ANVHFVGEVA	AFvDQIKKvL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_090}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_CJB110}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_18RS21}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_2603}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_COH1}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_M781}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVdaF
msa521982.2{69_1169NT}	ANVHFVGEVA	AFvDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMeSVNVdaF
msa521982.2{69_M732}	ANVHFVGEVA	AFfDQIKKaL	PHAKITETLP	CAVAIGRKGQ	KMkSVNVxxcF
Consensus	*****	**_*****_*	*****	*****	**_*****_*
201					
msa521982.2{69_A909}	VPRYLKRVEA	EENWLNHCE	TN-----		
msa521982.2{69_H36B}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_JM9130013}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_090}	VPRYLKRVEA	EENWLNHCE	TN-----		
msa521982.2{69_CJB110}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_18RS21}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_2603}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_COH1}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_M781}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_1169NT}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
msa521982.2{69_M732}	VPRYLKRVEA	EENWLNHCE	TNTEEYIKRV		
Consensus	*****	*****	*****		
230					

Table 85: Comparative Sequences relating to SAG1361

SEQ ID NO. 8501

STRAIN 2603

atgagtaaacgcaaaaatttaggaattagtaaaaaaggagcaattatatacagggctctca
gtggcactaatgttagtaaataggtggctttttatgggtacaatctcaacctaatagagt
gcagtaaaaactaactacaaagtttttaaagttagagaaggaggtgttcgtcctcaact
cttttgacagaaaagctaaaggctaatcaagaacagtatgtgtattttgatgctataaa
ggtaatcgagcaactgtcacagttaaagtgggtgataaaatcacagctggctcagcagtta
gttcaabatgatacaacaactgcacaagcagcctacgacactgctaatcgtcaattaaat
aaagttagcgcgtcagattataatcctaagacaacaggaagcttccagctatggaatca
agtgatcaatctcttcatcatcacaaggacaagggactcaatcgactagtggtgagcagc
aatcgtctacagcaaaattatcaaagcaagctaatgcttcatacaaccaacaactcaaa
gatttgaaatgatgcttatgcagatgcacaggcagagaagtaataaagcacaanaagcattg
aatgatactgttattacaagtgcagctacagggacagttgttgaagttaatagtgatatt
gatccagcttcaaaaactagtcaagtaactgtccatgtagcaactgaaggtaaaactcaaa
gtacaaggaacagatgagtgagatgatttggctaatgttaaaaaagaccaggctgttaaa
ataaaatctaaggtctatcctgacaaggaatgggaaggtaaaatttcatatctcaaat
tatccagaagcagaagcaacaacaatgactctaataacggctctagtgtgtaaatat
aaatataaagttagattactagccctctcgatgcattaaaacaaggtttaccgctatca
gttgaagtagttaaaggagataagcaccttatgtccctacaagttctgtgataaacaana
gataataaacactttgtttgggtatacaatgattctaatcgtaaaatttccaaagttgaa
gtcaaaattggtaagctgatgctaaagacacaagaattttatcaggttgaagcagga
caaatcgtggttactaatccaagtaaaccttcaaggatgggcaaaaaattgataatatt
gaatcaatcgatcttaactctaataagaatcagaggtgaaa

SEQ ID NO. 8502

STRAIN 090

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCAAGTTAAAGTGGTGATAAAATCACAGC
TGCTCAGCAGTTAGTTCATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGGCAGCAATCGTC
TACAGCAAAATATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
CAAGATTTGAATGATGCTTATGACAGTGCACAGGCAGAAAGTAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTAACAAGTACGCTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTCA
CTTGTCCATGTAGCAACTGAAGGTAACCTCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAGACCAGGCTGTTAAAAATAAAT
CTAAGGTCTATCCTGACAAGGAATGGGAAGGTAATAATTCATATATCTCA
AATTAATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAATTAATAATATAAAGTAGATATTAAGTCCCTCTCGATGCAT
TAAAACAAGGTTTTACCGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTCCCTACAAGTTCTGTGATAAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATTTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
GGACAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG

SEQ ID NO. 8503

STRAIN A909

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAA
CTACAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTT
TGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCT
AATAAAGGTAATCGAGCAACTGTTACAGTTAAAGTGGTGATAAAATCAC
AGCTGGTCAGCAGTTAGTTCATATGATACAACAACCTGCACAAGCAGCCT
ACGCACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAAT
CTAAAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTC
ATCATCTACAAGGACAAGGGCTCAATCGACTAGTGGTGGCAGCAATC
GTCTACAGCAAAATATCAAAGTCAAGCTAATGCTTCATACAACCAACA
CTTCAAGATTTGAATGATGCTTATGACAGTGCACAGGCAGAAAGTAATAA
AGCAAAAAGCATTGAATGATACTGTTATTAACAAGTACGCTATCAGGGA
CAGTTGTTGAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTCA
GTACTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGAT
GAGTGATGATGATTTGGCTAATGTTAAAAAGACCAGTCTGTTAAAAATA
AATCTAAGGTCTATCCTGACAAGGAATGGGAAGGTAATAATTCATATATC
TCAAATTAATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTC
TAGTGCTGTAATAATATAAATATAAAGTAGATATTAAGTCCCTCTCGATG
CATTAACAACAAGTTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAG
CACCTTATGTTCTACAAGTTCTGTGACAAAACAAGATAATAAACACTT
TGTTGGGTATACAATGATTTAATCGTAAAAATTTCCAAAGTTGAAGTCA
AAATTTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAG
GCAGGACAAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCA
AAAAATTGATAATATTGAATCAATAGATCTTAAGTCTAATAAGAAATCAG
AGGTGAAA

SEQ ID NO. 8504

STRAIN H36B

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTTAAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAGGGTAATCGAGCAACTGTACAGTTAAAGTGGTGATAAAATCACAGC

Table 85: Comparative Sequences relating to SAG1361

TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTAATCAAAGTCAAGCTAATGCTTCATACAACCAACTT
CAAGATTGAAATGATGCTTATGAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTCAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTAATAAAGACCAAGGCTGTTAAATAAAT
CTAAGGCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
AATTAATCCAGAAGCAGAAGCAACAACCAATGACTCTAATAACGGCTCTAG
TGCTGTAATTAATAATAAAGTAGATATTAAGTCCCTCTCGATGCAT
TAAAACAAGGTTTACTGTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTTCTACAAGTTCTGTGACAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
GGACAATCGTAGTTACTAATCCAAGTAAAGCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TG

SEQ ID NO. 8505
STRAIN 18RS21

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCAAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTTCCAGCTATGGAATCAAGTGAATCAATCTTCTC
ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTAATCAAAGTCAAGCTAATGCTTCATACAACCAACTT
CAAGATTGAAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTGAAGTATCAGGGACAG
TTGTTCAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAAGGCTGTTAAATAAAT
CTAAGGCTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
AATTAATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAATTAATAATAAAGTAGATATTAAGTCCCTCTCGATGCAT
TAAAACAAGGTTTACCCTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
GGACAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAG

SEQ ID NO. 8506
STRAIN M732

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGGAGTTTCCAGCTATGGAATCAAGTGAATCAATCTTCTC
ATCATACAAGGACAAGGACTCAATCGACTAGTGGTGCGACGAATCGTC
TACAGCAAAATTAATCAAAGTCAAGCTAATGCTTCATACAACCAACTT
CAAGATTGAAATGATGCTTATGCAGATGCACAGGCAGAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTGAAGTATCAGGGACAG
TTGTTCAAGTTAATAGTGATATGATCCAGCTTCAAAAAGTCAAGTCAAGTA
CTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTTAAATAAAT
CTAAGGCTCTATCCTGACAAGGAATGGGAAGGTAAATTTTCATATATCTCA
AATTAATCCAGAAGCAGAAGCAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAATTAATAATAAAGTAGATATTAAGTCCCTCTCGATGCAT
TAAAACAAGGTTTACCCTATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTTCCCTACAAGTTCTGTGATAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATTCTAATCGTAAAAATTTCCAAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGCA
GGACAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGGCAAAA
AATTGATAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8507
STRAIN COH1

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAAAC
TAATTAACAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTC
TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGA
GCTAATAAAGGTAATCGAGCAACTGTACAGTTAAAGTGGGTGATAAAAT
CACAGCTGGTCAGCAGTTAGTTCAATATGATACAACTGCACAAGCAG
CCTACGACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAAT
AATCTAAAGACAACAGGAGTTTCCAGCTATGGAATCAAGTGAATCAATC

Table 85: Comparative Sequences relating to SAG1361

TTCATCATCATCACAAGGACAAGGGACTCAATCGACTAGTGGTGCGACGA
ATCGTCTACAGCAAAAATATCAAAGTCAAGCTAATGCTTCATACAACCAA
CAACTTCAAAGATTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAA
TAAAGCACA AAAAGCATGAATGATACTGTATTACAAGTGACGTATCAG
GGACAGTTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAC TAGT
CAAGTACTTGTCCATGTAGCAACTGAAGGTAAACTCCAAGTACAAGGAAC
GATGAGTGAATGATGATTGGCTAATGTAAAAAAGATCAGGCTGTAAAAA
TAAAATCTAAGGCTATCTCTGACAAGGAATGGGAAGGTAAAAATTCATAT
ATCTCAAATATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGG
CTCTAGTGTCTGTAATATAAATATAAAGTAGATATTACTAGCCCTCTCG
ATGCATTA AAAACAAAGGTTTACCCTGATCAGTTGAAGTAGTTAATGGAGAT
AAGCACCCTTATTGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACA
CTTTGTTTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAG
TCAAAAATGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTG
AAAGCAGGACAAATCGTGGTTACTAATCCAAGCAAAAATTTCAAGGATGG
GCAAAAATTGATAAATTTGAATCAATCGATCTTAAGTCTAATAAGAAAT
CAGAGGTGAA

SEQ ID NO. 8507

STRAIN M781

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAATTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTTACAGTTAAAAGTGGGTGATAAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGGAGTTTTCCAGCTATGGAATCAAGTGATCAATCTTCATC
ATCATACAAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
TACAGCAAAAATATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCT
CAAGATTTGAATGATGCTTATGAGATGCACAGGCAGAAAGTAATAAAGC
ACAAAAGCAATGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAC TAGTCAAGTA
CTGTCCATGTAGCAACTGAAGGTAACCTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGATCAGGCTGTAAAAATAAAT
CTAAGTCTATCTGACAAGGAATGGGAAGTAAAATTTTCATATATCTCA
AATTAATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAAATATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCCTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACAACCTTTGT
TTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAATCGTGGTTACTAATCCAAGCAAAAATTTCAAGGATGGGCAAAA
AATTGATAAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGAA

SEQ ID NO. 8508

STRAIN CJB110

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATGCTAAT
AAAGGTAATCGAGCAACTGTCACAGTTAAAAGTGGGTGATAAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTCCAGCTATGGAATTAAGTGATCAATCTTCTTC
ATCATACAAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAATCGTC
TACAGCAAAAATATCAAAGTCAAGCTAATGCTTCATACAACCAACAACCTT
CAAGATTTGAATGATGCTTATGAGATGCACAGGCAGAAAGTAATAAAGC
ACAAAAGCAATGAATGATACTGTTATTACAAGTGACGTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTGATCCAGCTTCAAAAAC TAGTCAAGTA
CTGTCCATGTAGCAACTGAAGGTAACCTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAAGACCAGGCTGTAAAAATAAAT
CTAAGTCTATCTGACAAGGAATGGGAAGGTAAAATTTTCATATATCTCA
AATTAATCCAGAAGCAGAAGCAAACAACAATGACTCTAATAACGGCTCTAG
TGCTGTAAAATATAAATATAAAGTAGATATTACTAGCCCTCTCGATGCAT
TAAAACAAGGTTTTACCCTGATCAGTTGAAGTAGTTAATGGAGATAAGCAC
CTTATGTCCCTACAAGTTCTGTGATAAACAAGATAATAAACAACCTTTGT
TTGGGTATACAATGATTTCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAAGCA
GGACAATCGTGGTTACTAATCCAAGTAAAACCTTCAAGGATGGGCAAAA
AATTGATAAATATTGAATCAATCGATCTTAAGTCTAATAAGAAATCAGAGG
TGA

SEQ ID NO. 8509

STRAIN 1169NT

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACT
AACTACAAGTTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCT
TTTTGACAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGTATTTTGATG
CTAATAAAGGTAATCGAGCAACTGTCACAGTTAAAAGTGGGTGATAAAAATC
ACAGCTGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGC
CTACGACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATA
ATCTAAAGACAACAGGAAGTCTCCAGCTATGGAATCAAGTGATCAATCT
TCTTCATCATACAAGGACAAGGGACTCAATCGACTAGTGGTGCAGCAAG
TCGCTACAGCAAAAATATCAAAGTCAAGCTAATGCTTCATACAACCAAC

Table 85: Comparative Sequences relating to SAG1361

AACCTCAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAAT
AAAGCACAAAAGCATTGAATGATACTGTTATTACAAGTGACGATCAGG
GACAGTTGTTGAAGTTAATAGTGATATTTGATCCAGCTTCAAAAAGTACGTC
AAGTACTTGTCCATGTAGCAACTGAAGGTAACCTCCAAGTACAAGGAACG
ATGAGTGAATGATGATTTGGCTAATGTTAAAAAGACCAGGCTGTTAAAT
AAAATCTAAGGCTATCTGACAAGGAATGGGAAGGTAATAATTTTCATATA
TCTCAAATATCCAGAAGCAGAAGCAAACAACAAATGACTCTAATAACGGC
TCTAGTGTGTAATATAAATAAAGTAGATATTAAGTACCTAGCCCTCTCGA
TGCATTAACAAGGTTTACCGTATCAGTTGAAGTAGTTAATGGAGATA
AGCACCTTATTTGTCCTACAAGTTCTGTGATAACAAGATAATAAACAC
TTTGTGTTGGGTATACAATGATCTAATCGTAAAAATTTCCAAGTTGAAGT
CAAAATTTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGA
AAGCAGGACAAATCGTGGTTACTAATCCAAGTAAACCTTCAAGGATGGG
CAAAAATTTGATAATATTTGAATCAATCGATCTTAACTCTAATAAGAAATC
AGAGGTGAA

SEQ ID NO. 8510
STRAIN JM9130013

TTTTTATGGGTACAATCTCAACCTAATAAGAGTGCAGTAAAACTAACTA
CAAAGTTTTAATGTTAGAGAAGGAAGTGTTCGTCCTCAACTCTTTTGA
CAGGAAAAGCTAAGGCTAATCAAGAACAGTATGTGATTTTGTGCTAAT
AAAGTAAATCGAGCAACTGTTACAGTTAAAGTGGGTGATAAAATCACAGC
TGGTCAGCAGTTAGTTCAATATGATACAACAACCTGCACAAGCAGCCTACG
ACACTGCTAATCGTCAATTAATAAAGTAGCGCGTCAGATTAATAATCTA
AAGACAACAGGAAGTCTCCAGCTATGGAAATCAAGTATCAATCTTCATC
ATCATCAAGGACAAGGGGCTCAATCGACTAGTGGTGGCAGCAATCGTC
TACGCAAAAATTTACAAGTCAAGCTAATGCTTCATACAACCAACAATCT
CAAGATTTGAATGATGCTTATGCAGATGCACAGGCAGAAAGTAAATAAAGC
ACAAAAGCATTGAATGATACTGTTATTACAAGTACGCTATCAGGGACAG
TTGTTGAAGTTAATAGTGATATTTGATCCAGCTTCAAAAAGTCAAGTCA
CTTGTCCATGTAGCAACTGAGGGTAAACTCCAAGTACAAGGAACGATGAG
TGAGTATGATTTGGCTAATGTTAAAAAGACCAGTCTGTTAAAATAAAT
CTAAGGTCTATCTGACAAGGAATGGGAAGGTAATAATTTTCATATATCTCA
AATTATCCAGAAGCAGAAGCAAACAACAAATGACTCTAATAACCGCTCTAG
TGCTGTAATTTATAAATAAAGTAGATATTAAGTACCTCTCGATGCAT
TAAAACAAGGTTTACTGTATCAGTTGAAGTATGTTAATGGAGATAAGCAC
CTTATTTGTTCTTACAAGTTCTGTGACAAAACAAGATAATAAACACTTTGT
TTGGGTATACAATGATCTAATCGTAAAAATTTCCAAGTTGAAGTCAAAA
TTGGTAAAGCTGATGCTAAGACACAAGAAATTTTATCAGGTTTGAAGACA
GGACAATCGTGGTTACTAATCCAAGCAAACTTCAAGGATGGGCAAAA
AATTGATAATATTTGAATCAATAGATCTTAAAGTCTAATAAGAAATCAGAGG
TGAAA

PRETTY of: /biotmp/msa363690.2{*} March 31, 2003 07:01 ..

msa363690.2{690_COH1}
msa363690.2{690_M732}
msa363690.2{690_M781}
msa363690.2{690_090}
msa363690.2{690_CJB110}
msa363690.2{690_1169NT}
msa363690.2{690_18RS21}
msa363690.2{690_2603}
msa363690.2{690_A909}
msa363690.2{690_JM9130013}
msa363690.2{690_H36B}
Consensus

msa363690.2{690_COH1}
msa363690.2{690_M732}
msa363690.2{690_M781}
msa363690.2{690_090}
msa363690.2{690_CJB110}
msa363690.2{690_1169NT}
msa363690.2{690_18RS21}
msa363690.2{690_2603}
msa363690.2{690_A909}
msa363690.2{690_JM9130013}
msa363690.2{690_H36B}
Consensus

msa363690.2{690_COH1}
msa363690.2{690_M732}
msa363690.2{690_M781}
msa363690.2{690_090}
msa363690.2{690_CJB110}
msa363690.2{690_1169NT}
msa363690.2{690_18RS21}
msa363690.2{690_2603}
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT
AATCTCAACC TAATAAGAGT GCAGTAAAAA CTAATACAA AGTTTTTAAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_A909}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_JM9130013}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
msa363690.2{690_H36B}	AATCTCAACC	TAATAAGAGT	GCAGTAAAAA	CTAAcTACAA	AGTTTTTAAAT
Consensus	*****	*****	*****	****-*****	*****
	151				200
msa363690.2{690_COH1}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_M732}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_M781}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_090}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_CJB110}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_1169NT}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_18RS21}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_2603}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_A909}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_JM9130013}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
msa363690.2{690_H36B}	GTTAGAGAAG	GAAGTGTTC	GTCCTCAACT	CTTTTGACAG	GAAAAGCTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa363690.2{690_COH1}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M732}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_M781}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_090}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_CJB110}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_1169NT}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_18RS21}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_2603}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_A909}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_JM9130013}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
msa363690.2{690_H36B}	GGCTAATCAA	GAACAGTATG	TGTATTTTGA	TGCTAATAAa	GGTAATCGAG
Consensus	*****	*****	*****	*****	*****
	251				300
msa363690.2{690_COH1}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M732}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_M781}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_090}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_CJB110}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_1169NT}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_18RS21}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_2603}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_A909}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_JM9130013}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
msa363690.2{690_H36B}	CAACTGTtAC	AGTTAAAGTG	GGTGATAAAA	TCACAGCTGG	TCAGCAGTTA
Consensus	*****	*****	*****	*****	*****
	301				350
msa363690.2{690_COH1}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M732}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_M781}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_090}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_CJB110}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_1169NT}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_18RS21}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_2603}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_A909}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_JM9130013}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
msa363690.2{690_H36B}	GTTCAATATG	ATACAACAAC	TGCACAAGCA	GCCTACGACA	CTGCTAATCG
Consensus	*****	*****	*****	*****	*****
	351				400
msa363690.2{690_COH1}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M732}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_M781}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_090}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_CJB110}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_1169NT}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_18RS21}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_2603}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_A909}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_JM9130013}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
msa363690.2{690_H36B}	TCAATTAAT	AAAGTAGCGC	GTCAGATTAA	TAATCTAAAG	ACAACAGGgA
Consensus	*****	*****	*****	*****	*****
	401				450
msa363690.2{690_COH1}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA
msa363690.2{690_M732}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA
msa363690.2{690_M781}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA
msa363690.2{690_090}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA
msa363690.2{690_CJB110}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA
msa363690.2{690_1169NT}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA
msa363690.2{690_18RS21}	GTTtTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcATC	ATCACAAGGA

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_2603}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcTcTcATC	ATCACAAGGA
msa363690.2{690_A909}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcCaTcATC	ATCACAAGGA
msa363690.2{690_JM9130013}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcCaTcATC	ATCACAAGGA
msa363690.2{690_H36B}	GTcTTCCAGC	TATGGAATcA	AGTGATCAAT	CTTcCaTcATC	ATCACAAGGA
Consensus	**_*****	*****_*	*****	****_****	*****
	451				500
msa363690.2{690_COH1}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M732}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_M781}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_090}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_CJB110}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_1169NT}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_18RS21}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_2603}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_A909}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_JM9130013}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
msa363690.2{690_H36B}	CAAGGGaCTC	AATCGACTAG	TGGTGCGACG	AATCGTCTAC	AGCAAAATTA
Consensus	*****_***	*****	*****	*****	*****
	501				550
msa363690.2{690_COH1}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_M732}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_M781}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_090}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_CJB110}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_1169NT}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_18RS21}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_2603}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_A909}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_JM9130013}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
msa363690.2{690_H36B}	TCAAAGTCAA	GCTAATGCTT	CATACAACCA	ACAACCTCAA	GATTTGAATG
Consensus	*****	*****	*****	*****	*****
	551				600
msa363690.2{690_COH1}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M732}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_M781}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_090}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_CJB110}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_1169NT}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_18RS21}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_2603}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_A909}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_JM9130013}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
msa363690.2{690_H36B}	ATGCTTATGC	AGATGCACAG	GCAGAAGTAA	ATAAAGCACA	AAAAGCATTG
Consensus	*****	*****	*****	*****	*****
	601				650
msa363690.2{690_COH1}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M732}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_M781}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_090}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_CJB110}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_1169NT}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_18RS21}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_2603}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_A909}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_JM9130013}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
msa363690.2{690_H36B}	AATGATACTG	TTATTACAAG	TGACGTATCA	GGGACAGTTG	TTGAAGTTAA
Consensus	*****	*****	*****	*****	*****
	651				700
msa363690.2{690_COH1}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M732}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_M781}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_090}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_CJB110}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_1169NT}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_18RS21}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_2603}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_A909}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_JM9130013}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
msa363690.2{690_H36B}	TAGTGATATT	GATCCAGCTT	CAAAAACCTAG	TCAAGTACTT	GTCCATGTAG
Consensus	*****	*****	*****	*****	*****
	701				750
msa363690.2{690_COH1}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M732}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_M781}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_090}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_CJB110}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_1169NT}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_18RS21}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_2603}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_A909}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_JM9130013}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
msa363690.2{690_H36B}	CAACTGAaGG	TAAACTCCAA	GTACAAGGAA	CGATGAGTGA	GTATGATTTG
Consensus	*****-**	*****	*****	*****	*****
751					
msa363690.2{690_COH1}	GCTAATGTtA	AAAAAGAtCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M732}	GCTAATGTtA	AAAAAGAtCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_M781}	GCTAATGTtA	AAAAAGAtCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_090}	GCTAATGTtA	AAAAAGAcCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_CJB110}	GCTAATGTtA	AAAAAGAcCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_1169NT}	GCTAATGTtA	AAAAAGAcCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_18RS21}	GCTAATGTtA	AAAAAGAcCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_2603}	GCTAATGTtA	AAAAAGAcCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_A909}	GCTAATGTtA	AAAAAGAcCA	GtCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_JM9130013}	GCTAATGTtA	AAAAAGAcCA	GtCTGTtAA	ATAAAATCTA	AGGTCTATCC
msa363690.2{690_H36B}	GCTAATGTtA	AAAAAGAcCA	GgCTGTtAA	ATAAAATCTA	AGGTCTATCC
Consensus	*****-*	*****-*	*-*****	*****	*****
801					
msa363690.2{690_COH1}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M732}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_M781}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_090}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_CJB110}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_1169NT}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_18RS21}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_2603}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_A909}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_JM9130013}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
msa363690.2{690_H36B}	TGACAAGGAA	TGGGAAGGTA	AAATTTcATA	TATCTCAAAT	TATCCAGAAG
Consensus	*****	*****	*****	*****	*****
851					
msa363690.2{690_COH1}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_M732}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_M781}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_090}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_CJB110}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_1169NT}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_18RS21}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_2603}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_A909}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_JM9130013}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
msa363690.2{690_H36B}	CAGAAGCAAA	CAACAATGAC	TCTAATAACG	GCTCTAGTGC	TGTAAAATTAT
Consensus	*****	*****	*****	*****	*****
901					
msa363690.2{690_COH1}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M732}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_M781}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_090}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_CJB110}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_1169NT}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_18RS21}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_2603}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_A909}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_JM9130013}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
msa363690.2{690_H36B}	AAATATAAAG	TAGATATTAC	TAGCCCTCFC	GATGCATTAA	AACAAGGTTT
Consensus	*****	*****	*****	*****	*****
951					
msa363690.2{690_COH1}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M732}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_M781}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_090}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_CJB110}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_1169NT}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_18RS21}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_2603}	TACcGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_A909}	TACTGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_JM9130013}	TACTGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
msa363690.2{690_H36B}	TACTGTATCA	GTTGAAGTAG	TTAATGGAGA	TAAGCACCTT	ATTGTcCCTA
Consensus	***-*****	*****	*****	*****	*****
1001					
msa363690.2{690_COH1}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_M732}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_M781}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_090}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT
msa363690.2{690_CJB110}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTGTTTG	GGTATACAAT

Table 85: Comparative Sequences relating to SAG1361

msa363690.2{690_1169NT}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACITTTGTTTG	GGTATACAAT
msa363690.2{690_18RS21}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTGTTG	GGTATACAAT
msa363690.2{690_2603}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTGTTG	GGTATACAAT
msa363690.2{690_A909}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTGTTG	GGTATACAAT
msa363690.2{690_JM9130013}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTGTTG	GGTATACAAT
msa363690.2{690_H36B}	CAAGTTCTGT	GATAAACAAA	GATAATAAAC	ACTTTTGTGTTG	GGTATACAAT
Consensus	*****	***-*****	*****	*****	*****
	1051				1100
msa363690.2{690_COH1}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_M732}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_M781}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_090}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_CJB110}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_1169NT}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_18RS21}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_2603}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_A909}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_JM9130013}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
msa363690.2{690_H36B}	GATTCTAATC	GTAAAAATTC	CAAAGTTGAA	GTCAAAATTG	GTAAGCTGA
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa363690.2{690_COH1}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M732}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_M781}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_090}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_CJB110}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_1169NT}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_18RS21}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_2603}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_A909}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_JM9130013}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
msa363690.2{690_H36B}	TGCTAAGACA	CAAGAAATTT	TATCAGGTTT	GAAAGCAGGA	CAATCGTgG
Consensus	*****	*****	*****	*****	*****-*
	1151				1200
msa363690.2{690_COH1}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M732}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_M781}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_090}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_CJB110}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_1169NT}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_18RS21}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_2603}	TTACTAATCC	AAGtAAAaCc	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_A909}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_JM9130013}	TTACTAATCC	AAGcAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
msa363690.2{690_H36B}	TTACTAATCC	AAGtAAAaCt	TTCAAGGATG	GGCAAAAAAT	TGATAATATT
Consensus	*****	***-***-*	*****	*****	*****
	1201				1242
msa363690.2{690_COH1}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M732}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_M781}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_090}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGg---	--
msa363690.2{690_CJB110}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGgtga	--
msa363690.2{690_1169NT}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGgtga	a-
msa363690.2{690_18RS21}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAG---	--
msa363690.2{690_2603}	GAATCAATcG	ATCTTAAcTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_A909}	GAATCAATaG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_JM9130013}	GAATCAATaG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtga	aA
msa363690.2{690_H36B}	GAATCAATcG	ATCTTAAgTC	TAATAAGAAA	TCAGAGgtg-	--
Consensus	*****-*	*****-*	*****	*****	*****-***

SEQ ID NO. 8511
 STRAIN 2603 frame: 1
 MSKRQNLGI SKKGAI ISGLSVALIVVIGGFLWVQSQPNSAVKTNKYVFNVREGSVSSST
 LLTGKAKANQEYVYFDANKGNRATVTVKVGDKITAGQQLVQYDITTAQAAYDTANRQLN
 KVARQINNLKTTGSLPAMESSDQSSSSQGGTQSTSGATNRLQONYQSQANASYNQQLQ
 DLNDAYADAQAEVNKAQKALNDTVITSDVSGTVVEVNSDIDPASKTSQLVHVHATEGKLG
 VQGTMSYDLANVKKQAVKI KSKVYYPDKWEWEGKISYISNYPEAEANNNDNSNGSSAVNY
 KYKVDITSPLDALKQGFVTSVEVNGDKHLIVPTSSVINKNKHFVWVYVNDNSNRKISKVE
 VKIGKADAKTQEILSGLKAGQIVVTNPSKTFKDGQKIDNIESIDLNSNKKSEVK

SEQ ID NO. 8512
 STRAIN 090 frame: 1
 FLWVQSQPNSAVKTNKYVFNVREGSVSSSTLLTGKAKANQEYVYFDANKGNRATVTVK
 VGDKITAGQQLVQYDITTAQAAYDTANRQLNVARQINNLKTTGSLPAMESSDQSSSSSQ
 GGTQSTSGATNRLQONYQSQANASYNQQLQDLNDAYADAQAEVNKAQKALNDTVITSDV
 SGTVVEVNSDIDPASKTSQLVHVHATEGKLGQVQGTMSYDLANVKKQAVKI KSKVYYPDK
 WEWEGKISYISNYPEAEANNNDNSNGSSAVNYKYKVDITSPLDALKQGFVTSVEVNGDKH
 LIVPTSSVINKNKHFVWVYVNDNSNRKISKVEVKIGKADAKTQEILSGLKAGQIVVTNPSK
 TFKDGQKIDNIESIDLNSNKKSE

Table 85: Comparative Sequences relating to SAG1361

msa375805.2{690_CJB110}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
msa375805.2{690_1169NT}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
msa375805.2{690_18RS21}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
msa375805.2{690_2603}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
msa375805.2{690_A909}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
msa375805.2{690_JM9130013}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
msa375805.2{690_H36B}	NDTVITSDVSV	GTVVEVNSDI	DPASKTSQVVL	VHVATEGKQLQ	VQGTMSSEYDL
Consensus	*****	*****	*****	*****	*****
	251				300
msa375805.2{690_COH1}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M732}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_M781}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_090}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_CJB110}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_1169NT}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_18RS21}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_2603}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_A909}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_JM9130013}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
msa375805.2{690_H36B}	ANVKKDQaVK	IKSKVYPDKE	WEGKISYISN	YPEAEANNND	SNNGSSAVNY
Consensus	*****	*****	*****	*****	*****
	301				350
msa375805.2{690_COH1}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_M732}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_M781}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_090}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_CJB110}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_1169NT}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_18RS21}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_2603}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_A909}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_JM9130013}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
msa375805.2{690_H36B}	KYKVDITSPL	DALKQGFTVS	VEVVNGDKHL	IVPTSSVINK	DNKHFVWVYN
Consensus	*****	*****	*****	*****	*****
	351				400
msa375805.2{690_COH1}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M732}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_M781}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_090}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_CJB110}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_1169NT}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_18RS21}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_2603}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_A909}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_JM9130013}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKT	FKDGQKIDNI
msa375805.2{690_H36B}	DSNRKISKVE	VKIGKADAKT	QEILSGLKAG	QIVVTNPSKa	FKDGQKIDNI
Consensus	*****	*****	*****	*****	*****
	401		414		
msa375805.2{690_COH1}	ESIDLkSNKK	SEv-			
msa375805.2{690_M732}	ESIDLkSNKK	SEv-			
msa375805.2{690_M781}	ESIDLkSNKK	SEv-			
msa375805.2{690_090}	ESIDLnSNKK	SE--			
msa375805.2{690_CJB110}	ESIDLnSNKK	SEv-			
msa375805.2{690_1169NT}	ESIDLnSNKK	SEv-			
msa375805.2{690_18RS21}	ESIDLnSNKK	SE--			
msa375805.2{690_2603}	ESIDLnSNKK	SEvK			
msa375805.2{690_A909}	ESIDLkSNKK	SEvK			
msa375805.2{690_JM9130013}	ESIDLkSNKK	SEvK			
msa375805.2{690_H36B}	ESIDLkSNKK	SEv-			
Consensus	*****	***			

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8601

STRAIN 2603

atgaaaaaaattggaattattgtcctcacactactgaccttcttttgggtatcttgcgga
caacaactaaacaagaagcactaaaacaactatttctaaaatgcctaaaattgaaggc
ttcacctattatggaaaaatcctgaaaatcggaaaaagtaatttttacatattct
tacactgggtatatttataaaactaggtgtaaatgtttcaagttacagtttagacttagaa
aaagatagcccggttttggtaaaacaactgaagaagctaaaaaattaactgctgatgat
acagaagctattgcccgcacaaaaacctgatttaaatcatgggttttcgatcaagatccaac
atcaatactctgaaaaaaattgcccacactttagttataaataggtgcaaaaaattat
ttagatgatgagcagccttggggaaaagtattcggtaaagaaaaagaagcattcagtggtg
gttagccaatggaaaaactaaaactctcgctgtcaaaaaagatttacaccatattcctaag
cctaacactacttttactattatggatttttatgataaaaaatctatttatatggtaaat
aatttggacgcggtggagaactaatctatgattcactaggttatgctgccccagaaaa
gtcaaaaaagatgtctttaaaggggtgggtttaccggttcgcaagaagcaatcgggtgat
tacgttggagattatgccccttggtaataataaacaacagactaaaaagcagcttcatca
cttaaagaagtgatgtctggaagaattaccagctgtcaaaaaaggccacatcatagaa
agtaactacgagctgttttatttctctgacctctatctttagaagctcaataaaaatca
tttacaaggctatcaagaaaaatacaaat

SEQ ID NO. 8602

STRAIN 090

GAAGGCTTCACCTATTATGGAAAAATTCCTGAAAATCCGAAAAAGTAAT
TAATTTTACATATTCTTACACTGGGTATTTATTAATACTAGGTGTTAATG
TTTCAAGTTACAGTTTAGACTTAGAAAAAGATAGCCCCGTTTTTGGTAAAG
CAACTGAAAGAGCTAAAAAATTAACCTGCTGATGATACAGAAGCTATTGCG
CGCACAAAAACCTGATTTAATCATGGTTTTTCGATCAAGATCCAAACATCA
ATACTCTGAAAAAATTCACCAACTTTAGTTATTAATATGGTGCACAA
AATTTATGATATGATGCGCAGCCTTGGGAAAAGTATTCGGTAAAGAAAA
AGAAGCTAATCAGTGGGTAGCCAATGGAAAACTAAAACCTCTCGCTGCCA
AAAAAGATTTACACCATATCTTAAAGCCTAACACTACTTTTACTATTATG
GATTTTATGATAAAAAATATCTATTTATATGGTAATAATTTTGGACCGGG
TGGAGAACTAATCTATGATTCCTAGGTATGCTGCCCAAGAAAAAGTCA
AAAAAGATGTCTTAAAAAAGGGTGGTTTACCCTTTCgCAAGAAGCAARTc
GGtGATTACGTTGGAGATTATGCCCTTGTAAATAAACAACAAACGACTAA
AAAAGCAGCTTCatcACTTAAAGAAAGTGATGTCTGGAAGAATTTACCAG
CTGTcaAAAAAGGGCACATCATAGAAAGTAAcTACGACGTGTTTTATTTC
TCTGACCTCTATCTTTAGAAGCTCAATTAATAATCATTTACAAA

SEQ ID NO. 8603

STRAIN A909

GAAGGCTTCACCTATTATGGAAAAATTCCTG
AAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGGATATTTA
TTAAAACCTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAAAAGA
TAGCCCCGTTTTTGGTAAaCAACTGAAAGGAGCTAAAAAATTAACCTGCTG
ATGATACAGAAGCTATTGCGGCACAAAAACCTGATTTAaTCATGGTTTTT
GATCAAGATCCAAACATCAATACTCTGAAAAAATTCACCAACTTTTAGT
TATTAATATGGTGCACAAAATTTATTTAgAtaTGATGCCAGCTTTGGGGA
AAGTATTCGGTAAAGAAAAAGGCTAATCAGTGGGTAGCCaTGGAAA
ACTAAAACCTCTCGCTGCCAAAAAAGATTACACCATATCTTAAAACCTAA
CACTACTTTTACCATTATGGATTTTATGATAAAAAATATCTATTTATATG
GTAATAATTTTGGACGGTGGAGAACTAATCTATGATTCACCTAGGTAT
GCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGTGGTTTTAC
CGTTTTCGCAAGAAAGCAATCGGTgATTACGTTGGAGATTATGCCCTTGTTA
ATATAACAACAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAGTAT
GTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAGAAAGTAA
CTACGACGTGTTTTATTCTCTGACCTcTATCTTTAGAAGCTCAATTA
AATCATTTACAAA

SEQ ID NO. 8604

STRAIN H36B

GAAGGCTTCACCTATTATGGAAAA
ATTCTGAAAATCCGAAAAAAGTAATTAATTTTACATATTCTTACACTGG
ATATTTATTAATAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGACTTAG
AAAAAGATagCCCCGTTTTTGGTAAgCAACTGAAAGGAGCTAAAAAATTA
ACTGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAaTCAT
GGTTTTTATGATCAAGATCCAAACATCAATACTCTGAAAAAATTCACCAA
CTTTAGTTATTAATATGGTGCACAAAATTTATTTAgAtaTGATGCCAGCT
TTGGGGAaAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTAGCCA
ATGGAAAACTAAAACCTCTCGCTGCCAAAAAAGATTACACCATATCTTAA
GGCCTaACACTACTTTTACTATTATAGAtTTTTATGATAAAAAATATCTAT
TTATATGGTAATAATTTTGGACGGGTGGAgAACTAATCTATGATcCACT
AGGTTATGCTGCCCCAgAAAAAGTCAAAAAAGATGTCTTTAAAAAAGGGT
GGTTTTACGTTTTcGCAAGAAGCAATCGGTgATTACGTTGGAGATTATGCC
CTTGTTAAATATAACAACAAACGACTAAAAAAGCAGCTTCaTCACTTAAAGA
AAGTGATGTTTTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCATAG
AAAGTAACACGACGTGTTTTATTCTCTGACCTCTATCTTTAGAAGCT
CAATTAATAATCATTTACAAA

Table 86: Comparative Sequences relating to SAG1393

SEQ ID NO. 8605
 STRAIN 18RS21
 GAAGGCTTCACCTATTATGGA
 AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
 TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
 TAGAAAAAGATAGCCCCGTTTTTGGTAACAACCTGAAAGAAGCTAAAAAA
 TTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAAT
 CATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTTGCAC
 CAACCTTAGTTATTAATAATGGTGCACAAAATTTTtagATaTGATGCCA
 GCCTTGGGGAAAGTATTTCGGTAAAGAAAAgAAGCTAATCAGTGGGTTAG
 CCAATGGAAAACAAAACTCTCGCTGTCAAAAAAGATTACACCATATCT
 TAAAGCCTAACACTACTTTTACTATTATGGATTTTATGATAAAAAATATC
 TATTTATATGGTAATAATTTTGACGCGGTGGAGAAC TAATCTATGATTC
 ACTAGGTTATGCTGCCCCagAAAAAGTCAAAAAgATGTCTTTAAAAAAG
 GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
 GCCCTTGTTAATATAAAACAAACgACTAAAAAAGCAGCTTCATCACTTAA
 AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATCA
 TAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGAA
 GCTCAATTAATAATCATTACAAA

SEQ ID NO. 8606
 STRAIN M732
 GAAGGCTTCACCTATTATGG
 AAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTTGCA
 CCAACCTTAGTTATTAATAATGGTGCACAAAATTTTtagATaTGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGCTAATCAGTGGGTTA
 GCCAATGGAAAACAAAACTCTCGCTGCCAAAAAAGATTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACgCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTA
 AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACATC
 ATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAGA
 AGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8607
 STRAIN COH1
 GAAGGCTTCACCTATTATG
 GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
 ACTGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTtagA
 CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAA
 AATTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTA
 ATCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTTGC
 ACCAACTTTAGTTATTAATAATGGTGCACAAAATTTTtagATaTGATGATG
 CAGCTTGGGGAAAGTATTcGGTAAAGAAAAAGCTAATCAGTGGGTT
 AGCCAATGGAAAACAAAACTCTCGCTGCCAAAAAAGATTTACACCATAT
 CTTAAAGCCTAACACTACTTTTACTATTATGGATTTTATGATAAAAAATA
 TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGAT
 TCAC TAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 AGGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATT
 ATGCCCTTGTTAATAATAAAACAAACGACTAAAAAAGCAGCTTCATCACTT
 AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAAGGGCACAT
 CATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCTCTATCTTTAG
 AAGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8608
 STRAIN M781
 GAAGGCTTCACCTATTATGG
 AAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACA
 CTGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGAC
 TTAgAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAA
 ATTAAC TGCTGATGATACAGAAGCTATTGCCGCACAAAAACCTGATTTAA
 TCATGGTTTTTCGATCAAGATCCAAACATCAATACTCTGAAAAAATTTGCA
 CCACTTTAGTTATTAATAATGGTGCACAAAATTTTtagATaTGATGATGCC
 AGCCTTGGGGAAAGTATTTCGGTAAAGAAAAAGCTAATCAGTGGGTTA
 GCCAATGGAAAACAAAACTCTCGCTGCCAAAAAAGATTTACACCATATC
 TTAAGCCTAACACTACTTTTACTATTATGGATTTTATGATAAAAAATAT
 CTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACTAATCTATGATT
 CACTAGGTTATGCTGCCCCAGAAAAAGTCAAAAAAGATGTCTTTAAAAA
 GGGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTA
 TGCCCTTGTTAATATAAAACAAACGACTAAAAAAGCAGCTTCATCACTTA

Table 86: Comparative Sequences relating to SAG1393

AAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATC
ATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCCTATCTTTTGA
AGCTCAATTAATAATCATTACAAA

SEQ ID NO. 8609

STRAIN CJB110

GAAGGCTTCACCTATTATGGA
AAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACAC
TGGGTATTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACT
TAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAA
TTAACTGCTGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTAAT
CATGGTTTTCGATCAAGATCCAAACATCAATACCTGAAAAAAATGGCAC
CAACTTAGTTATTAAATATGGTGCACAAAATTTTAgATATGATGCCA
GCCTTGGGGAAGTATTCGGTAAAGAAAAAGAGCTAATCAGTGGGTAG
CCAATGGAAAACTAAAACCTCGCTGCCAAAAAGATTACACCATATCT
TAAAGCCTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATC
TATTTATATGTTAATAATTTTGGACGCGGTGGAGAACAATCTATGATTC
ACTAGGTTATGCTGCCCGAGAAAAAGTCAAAAAGATGCTTTAAAAAAG
GGTGGTTTACCGTTTTCGCAAGAAGCAATCGGTGATTACGTTGGAGATTAT
GCCCTTGTAAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAA
AGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCA
TAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCCTATCTTTAGAA
GCTCAATTAATAATCATTACAAA

SEQ ID NO. 8610

STRAIN 1169NT

GAAGGCTTCACCTATTATGAAAAAATT
CCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTACACTGGGTA
TTTATTAATACTAGGTGTTAATGTTTCAAGTTACAGTTTAGACTTAGAAA
AAGATAGCCCCCGTTTTTGGTAAGCAACTGAAAGAAGCTAAAAAATTAAT
GCTGATGATACAGAAGCTATTGCCGCACAAAaACCTGATTTAATCATGGT
TTTCGATCAAGATCCAAACATCAATACCTGAAAAAAATGGCACCAACTT
TAGTTATTAATAATATGGTGCACAAAATTTTAgATATGATGCCACCTTG
GGGAAAGTATTCGGTAAAGAAAAAGaaGCTAATCAGTGGGTAGCCAATG
GAAAATAAACTCTCGCTGCCAAAAAGATTACACCATACTTAAAGC
CTAACACTACTTTTACTATTATGGATTTTTATGATAAAAATATCTATTTA
TATGGTAATAATTTTGGACGCGGTGGAGAACAATCTATGATTCAC TAGG
TTATGCTGCCCGAGAAAAAGTCAAAAAGATGCTTTAAAAAAGGGTGGT
TTACCGTTTTGCAAGAAGCAATCGGTGATTACGTTGGAGATTATGCCCTT
GTTAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTTAAAGAAAG
TGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACATCATAGAAA
GTAACTACGACGTGTTTTATTCTCTGACCCCTATCTTTAGAAGCTCAA
TTAAATCATTACAAA

SEQ ID NO. 8611

STRAIN JM9130013

GAAGGCTTCACCTATTATG
GAAAAATTCCTGAAAATCCGAAAAAGTAATTAATTTTACATATTCTTAC
ACTGGATATTATTAACTAGGAGTTAATGTTTCAAGTTACAGTTTAGA
CTTAGAAAAAGATAGCCCCGTTTTTGGTAAGCAACTGAAAGGAGCTAAAA
AATTAAGTGCATGATGATACAGAAGCTATTGCCGCACAAAACCTGATTTA
ATCATGGTTTTGATCAAGATCCAAACATCAATACCTGAAAAAAATTGC
ACCAACTTTAGTTATTAAATATGGTGCACAAAATTTTAgATATGATGC
CAGCTTTGGGGAAGTATTTCGGTAAAGAAAAAGAGCTAATCAGTGGGTT
AGCCAATGGAAAACATAAACTCTCGCTGCCAAAAAGATTACACCATAT
CTTAAACCTAACACTACTTTTACCATTATGGATTTTTATGATAAAAATA
TCTATTTATATGGTAATAATTTTGGACGCGGTGGAGAACAATCTATGAT
TCACTAGGTTATGCTGCCCGAGAAAAAGTCAAAAAGATGCTTTAAAAAA
AGGGTGGTTTTACCGTTTTGCAAGAAGCAATCGGTGATTACGTTGGAGATT
ATGCCCTTGTAAATATAACAAAACGACTAAAAAAGCAGCTTCATCACTT
AAAGAAAGTGATGTCTGGAAGAATTTACCAGCTGTCAAAAAGGGCACAT
CATAGAAAGTAACTACGACGTGTTTTATTCTCTGACCCCTATCTTTAG
AAGCTCAATTAATAATCATTACAAA

Pretty of: /biotmp/msa521731.2{*} April 28, 2003 08:07 ..

Table with 5 columns: sequence identifier, alignment line 1, alignment line 2, alignment line 3, alignment line 4. Row 1: msa521731.2{691_090} 1 50. Row 2: msa521731.2{691_1169NT}. Row 3: msa521731.2{691_CJB110}. Row 4: msa521731.2{691_COH1}. Row 5: msa521731.2{691_M732}. Row 6: msa521731.2{691_M781}. Row 7: msa521731.2{691_18RS21}. Row 8: msa521731.2{691_2603} atgaaaaaaa ttggaattat tgtcctcaca ctactgacct tctttttggt

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	51				100
msa521731.2{691_090}	-----	-----	-----	-----	-----
msa521731.2{691_1169NT}	-----	-----	-----	-----	-----
msa521731.2{691_CJB110}	-----	-----	-----	-----	-----
msa521731.2{691_COH1}	-----	-----	-----	-----	-----
msa521731.2{691_M732}	-----	-----	-----	-----	-----
msa521731.2{691_M781}	-----	-----	-----	-----	-----
msa521731.2{691_18RS21}	-----	-----	-----	-----	-----
msa521731.2{691_2603}	atcttgcgga	caacaaacta	aacaagaaag	cactaaaaca	actatttcta
msa521731.2{691_A909}	-----	-----	-----	-----	-----
msa521731.2{691_JM9130013}	-----	-----	-----	-----	-----
msa521731.2{691_H36B}	-----	-----	-----	-----	-----
Consensus	*****	*****	*****	*****	*****
	101				150
msa521731.2{691_090}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_1169NT}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_CJB110}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_COH1}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M732}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_M781}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_18RS21}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_2603}	aaatgcctaa	aattGAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_A909}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_JM9130013}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
msa521731.2{691_H36B}	-----	----GAAGGC	TTCACCTATT	ATGGAAAAAT	TCCTGAAAAAT
Consensus	*****	*****	*****	*****	*****
	151				200
msa521731.2{691_090}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_1169NT}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_CJB110}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_COH1}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M732}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_M781}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_18RS21}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_2603}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_A909}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_JM9130013}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
msa521731.2{691_H36B}	CCGAAAAAAG	TAATTAATTT	TACATATTCT	TACACTGGgT	ATTTATTAAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa521731.2{691_090}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_1169NT}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_CJB110}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_COH1}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M732}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_M781}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_18RS21}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_2603}	ACTAGGtGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_A909}	ACTAGGgGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_JM9130013}	ACTAGGgGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
msa521731.2{691_H36B}	ACTAGGgGTT	AATGTTTCAA	GTTACAGTTT	AGACTTAGAA	AAAGATAGCC
Consensus	*****	*****	*****	*****	*****
	251				300
msa521731.2{691_090}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_1169NT}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_CJB110}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_COH1}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M732}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_M781}	CCGTTTTTGG	TAAgCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_18RS21}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_2603}	CCGTTTTTGG	TAAaCAACTG	AAAGaAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_A909}	CCGTTTTTGG	TAAaCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_JM9130013}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
msa521731.2{691_H36B}	CCGTTTTTGG	TAAgCAACTG	AAAGgAGCTA	AAAAATTAAC	TGCTGATGAT
Consensus	*****	***-*****	****-*****	*****	*****
	301				350
msa521731.2{691_090}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_1169NT}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_CJB110}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_COH1}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M732}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_M781}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_18RS21}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_2603}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_A909}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_JM9130013}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
msa521731.2{691_H36B}	ACAGAAGCTA	TTGCCGCACA	AAAACCTGAT	TTAATCATGG	TTTTcGATCA
Consensus	*****	*****	*****	*****	****-*****

	351				400
msa521731.2{691_090}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_1169NT}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_CJB110}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_COH1}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M732}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_M781}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_18RS21}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_2603}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_A909}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_JM9130013}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
msa521731.2{691_H36B}	AGATCCAAAC	ATCAATACTC	TGAAAAAAT	TGCACCAACT	TTAGTTATTA
Consensus	*****	*****	*****	*****	*****

	401				450
msa521731.2{691_090}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_1169NT}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_CJB110}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_COH1}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_M732}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_M781}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_18RS21}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_2603}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_A909}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_JM9130013}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
msa521731.2{691_H36B}	AATATGGTGC	ACAAAATTAT	TTAGATATGA	TGCCAGCcTT	GGGGAAGTA
Consensus	*****	*****	*****	*****	*****

	451				500
msa521731.2{691_090}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_1169NT}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_CJB110}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_COH1}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_M732}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_M781}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_18RS21}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_2603}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_A909}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_JM9130013}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
msa521731.2{691_H36B}	TTCGGTAAAG	AAAAGAAGC	TAATCAGTGG	GTTAGCCAAT	GGAAAACATA
Consensus	*****	*****	*****	*****	*****

	501				550
msa521731.2{691_090}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_1169NT}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_CJB110}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_COH1}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M732}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_M781}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_18RS21}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_2603}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_A909}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_JM9130013}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
msa521731.2{691_H36B}	AACTCTCGCT	GcCAAAAAG	ATTTACACCA	TATCTTAAag	CCTAACACTA
Consensus	*****	*-*****	*****	*****	*****

	551				600
msa521731.2{691_090}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_1169NT}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_CJB110}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_COH1}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M732}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_M781}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_18RS21}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_2603}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_A909}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
msa521731.2{691_JM9130013}	CTTTTACTAT	TATgGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_H36B}	CTTTTACTAT	TATaGATTTT	TATGATAAAA	ATATCTATTT	ATATGGTAAT
Consensus	*****_**	***-*****	*****	*****	*****
	601				650
msa521731.2{691_090}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_1169NT}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_CJB110}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_COH1}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M732}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_M781}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_18RS21}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_2603}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_A909}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_JM9130013}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
msa521731.2{691_H36B}	AATTTTGGAC	GCGGTGGAGA	ACTAATCTAT	GATTCAC TAG	GTTATGCTGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa521731.2{691_090}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_1169NT}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_CJB110}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_COH1}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M732}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_M781}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_18RS21}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_2603}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_A909}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_JM9130013}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
msa521731.2{691_H36B}	CCCAGAAAAA	GTCAAAAAAG	ATGTCCTTAA	AAAAGGGTGG	TTTACCGTTT
Consensus	*****	*****	*****	*****	*****
	701				750
msa521731.2{691_090}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_1169NT}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_CJB110}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_COH1}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M732}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_M781}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_18RS21}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_2603}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_A909}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_JM9130013}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
msa521731.2{691_H36B}	CGCAAGAAGC	AATCGGTGAT	TACGTTGGAG	ATTATGCCCT	TGTTAATATA
Consensus	*****	*****	*****	*****	*****
	751				800
msa521731.2{691_090}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_1169NT}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_CJB110}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_COH1}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M732}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_M781}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_18RS21}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_2603}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_A909}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_JM9130013}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
msa521731.2{691_H36B}	AACAAAACGA	CTAAAAAAGC	AGCTTCATCA	CTTAAAGAAA	GTGATGTcTG
Consensus	*****	*****	*****	*****	*****_**
	801				850
msa521731.2{691_090}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_1169NT}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_CJB110}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_COH1}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M732}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_M781}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_18RS21}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_2603}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_A909}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_JM9130013}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
msa521731.2{691_H36B}	GAAGAATTTA	CCAGCTGTCA	AAAAGGGCA	CATCATAGAA	AGTAACTACG
Consensus	*****	*****	*****	*****	*****
	851				900
msa521731.2{691_090}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_1169NT}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_CJB110}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA
msa521731.2{691_COH1}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAATCA

Table 86: Comparative Sequences relating to SAG1393

msa521731.2{691_M732}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_M781}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_18RS21}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_2603}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_A909}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_JM9130013}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
msa521731.2{691_H36B}	ACGTGTTTTA	TTTCTCTGAC	CCTCTATCTT	TAGAAGCTCA	ATTAAAATCA
Consensus	*****	*****	*****	*****	*****

	901		930
msa521731.2{691_090}	TTTACAAA--	-----	-----
msa521731.2{691_1169NT}	TTTACAAA--	-----	-----
msa521731.2{691_CJB110}	TTTACAAA--	-----	-----
msa521731.2{691_COH1}	TTTACAAA--	-----	-----
msa521731.2{691_M732}	TTTACAAA--	-----	-----
msa521731.2{691_M781}	TTTACAAA--	-----	-----
msa521731.2{691_18RS21}	TTTACAAA--	-----	-----
msa521731.2{691_2603}	TTTACAAA	ctatacaaga	aaatacaaat
msa521731.2{691_A909}	TTTACAAA--	-----	-----
msa521731.2{691_JM9130013}	TTTACAAA--	-----	-----
msa521731.2{691_H36B}	TTTACAAA--	-----	-----
Consensus	*****	*****	*****

SEQ ID NO. 8612
 STRAIN 2603 frame: 1
 MKKIGIIVLTLTFFLVSCGQQTQESTKTTTISKMPKIEGFTYYGKIPENPKKVINFTYS
 YTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLTADDTEAIAAQKPDLMVFDQDPN
 INTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEANQVWSQWKTTLAVKDLHHILK
 PNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAPKVKKDVFKKGWFTVSQEAIGD
 YVGDYALVNIINKTTKKAASSLKESDVWKNLPAVKKGGHIESNYDVFFYFSDPLSLEAQLKS
 FTKAIKENTN

SEQ ID NO. 8613
 STRAIN 090 frame: 1
 EGFTYYGKIPENPKKVINFTYSYTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEAN
 QVWSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIINKTTKKAASSLKESDVWKNLPAVKKGGH
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8614
 STRAIN A909 frame: 1
 EGFTYYGKIPENPKKVINFTYSYTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEAN
 QVWSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIINKTTKKAASSLKESDVWKNLPAVKKGGH
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8615
 STRAIN H36B frame: 1
 EGFTYYGKIPENPKKVINFTYSYTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEAN
 QVWSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIINKTTKKAASSLKESDVWKNLPAVKKGGH
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8616
 STRAIN 18RS21 frame: 1
 EGFTYYGKIPENPKKVINFTYSYTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEAN
 QVWSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIINKTTKKAASSLKESDVWKNLPAVKKGGH
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8617
 STRAIN M732 frame: 1
 EGFTYYGKIPENPKKVINFTYSYTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEAN
 QVWSQWKTTLAAKDLHHILKPNNTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
 EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIINKTTKKAASSLKESDVWKNLPAVKKGGH
 IESNYDVFFYFSDPLSLEAQLKSFT

SEQ ID NO. 8618
 STRAIN COH1 frame: 1
 EGFTYYGKIPENPKKVINFTYSYTGYYLLKLGIVNVSSYSLDLEKDSPVFGKQKLEAKKLT
 DDTEAIAAQKPDLMVFDQDPNINTLKKIAPTFLVIKYGAQNYLDMMPALGKVFGEKEAN

Table 86: Comparative Sequences relating to SAG1393

QWVSQWKTTLAAKDLHHILKPNFTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIKNTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYSDPLSLEAQLKSFT

SEQ ID NO. 8619
STRAIN M781 frame: 1
EGFTYYGKIPENPKKVINFTYSYTG YLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT A
DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMPALGKVF GKEKEAN
QWVSQWKTTLAAKDLHHILKPNFTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIKNTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYSDPLSLEAQLKSFT

SEQ ID NO. 8620
STRAIN CJB110 frame: 1
EGFTYYGKIPENPKKVINFTYSYTG YLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT A
DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMPALGKVF GKEKEAN
QWVSQWKTTLAAKDLHHILKPNFTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIKNTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYSDPLSLEAQLKSFT

SEQ ID NO. 8621
STRAIN 1169NT frame: 1
EGFTYYGKIPENPKKVINFTYSYTG YLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT A
DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMPALGKVF GKEKEAN
QWVSQWKTTLAAKDLHHILKPNFTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIKNTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYSDPLSLEAQLKSFT

SEQ ID NO. 8622
STRAIN JM9130013 frame: 1
EGFTYYGKIPENPKKVINFTYSYTG YLLKLG VNVSSYSLDLEKDS PVFGKQLKEAKKLT A
DDTEAIAAQKPD LIMVFDQDPNINTLKKIAPT LVIKYGAQNYLDMPALGKVF GKEKEAN
QWVSQWKTTLAAKDLHHILKPNFTTFTIMDFYDKNIYLYGNFGRGGELIYDSLGYAAP
EKVKKDVFKKGWFTVSQEAIGDYVGDYALVNIKNTTKKAASSLKESDVWKNLPAVKKGHI
IESNYDVFFYSDPLSLEAQLKSFT

PRETTY of: /biotmp/msa522124.2{*} April 28, 2003 08:17 ..

msa522124.2{691_090} 1 50
msa522124.2{691_1169NT} -----EG FTYYGKIPEN
msa522124.2{691_CJB110} -----EG FTYYGKIPEN
msa522124.2{691_COH1} -----EG FTYYGKIPEN
msa522124.2{691_M732} -----EG FTYYGKIPEN
msa522124.2{691_M781} -----EG FTYYGKIPEN
msa522124.2{691_18RS21} -----EG FTYYGKIPEN
msa522124.2{691_2603} mkkigiivlt lltfflvscg qqtqgestkt tiskmpkieG FTYYGKIPEN
msa522124.2{691_A909} -----EG FTYYGKIPEN
msa522124.2{691_JM9130013} -----EG FTYYGKIPEN
msa522124.2{691_H36B} -----EG FTYYGKIPEN
Consensus *****

msa522124.2{691_090} 51 100
msa522124.2{691_1169NT} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_CJB110} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_COH1} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_M732} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_M781} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_18RS21} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_2603} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KeAKKLTADD
msa522124.2{691_A909} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KgAKKLTADD
msa522124.2{691_JM9130013} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KgAKKLTADD
msa522124.2{691_H36B} PKKVINFTYS YTG YLLKLG V NVSSYSLDLE KDSPVFGKQL KgAKKLTADD
Consensus *****

msa522124.2{691_090} 101 150
msa522124.2{691_1169NT} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_CJB110} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_COH1} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_M732} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_M781} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_18RS21} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_2603} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_A909} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV
msa522124.2{691_JM9130013} TEAIAAQKPD LIMVFDQDPN INTLKKIAPT LVIKYGAQNY LDMPALGKV

Table 86: Comparative Sequences relating to SAG1393

msa522124.2{691_H36B}	TEAIAAQKPD	LIMVFDQDPN	INTLKKIAPT	LVIKYGAQNY	LDMMPALGKV
Consensus	*****	*****	*****	*****	*****
	151				200
msa522124.2{691_090}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_1169NT}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_CJB110}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_COH1}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M732}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_M781}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_18RS21}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_2603}	FGKEKEANQW	VSQWKTKTTLA	vKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_A909}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_JM9130013}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
msa522124.2{691_H36B}	FGKEKEANQW	VSQWKTKTTLA	aKKDLHHILk	PNTTFTImDF	YDKNIYLYGN
Consensus	*****	*****	*****	*****	*****
	201				250
msa522124.2{691_090}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_1169NT}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_CJB110}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_COH1}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M732}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_M781}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_18RS21}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_2603}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_A909}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_JM9130013}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
msa522124.2{691_H36B}	NFGRGGELIY	DSLGYAAPEK	VKKDVFKKGW	FTVSQEAIGD	YVG DYALVNI
Consensus	*****	*****	*****	*****	*****
	251				300
msa522124.2{691_090}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_1169NT}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_CJB110}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_COH1}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_M732}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_M781}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_18RS21}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_2603}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_A909}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_JM9130013}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
msa522124.2{691_H36B}	NKTTKKAASS	LKESDVWKNL	PAVKKGHIE	SNYDVYFSD	PLSLEAQLKS
Consensus	*****	*****	*****	*****	*****
	301	310			
msa522124.2{691_090}	FT-----				
msa522124.2{691_1169NT}	FT-----				
msa522124.2{691_CJB110}	FT-----				
msa522124.2{691_COH1}	FT-----				
msa522124.2{691_M732}	FT-----				
msa522124.2{691_M781}	FT-----				
msa522124.2{691_18RS21}	FT-----				
msa522124.2{691_2603}	FTkaikentn				
msa522124.2{691_A909}	FT-----				
msa522124.2{691_JM9130013}	FT-----				
msa522124.2{691_H36B}	FT-----				
Consensus	*****				

Table 87: Comparative Sequences relating to SAG0645

SEQ ID NO. 8701
 STRAIN 2603
 ATGAAATATCGAAGAAGTTATTGTTTTCGGCTGCTGTT
 TTAACAATGGTGGCGGGTCAACTGTTGAACCGTAGCTCAGTTTGGCGACTGGAATGAGT
 ATTGTAAGAGCTGCAGAAGTGTCA CAAGAACGCCAGCGAAAACAACAGTAAATATCTAT
 AAATTACAAGCTGATAGTTATAAATCGGAAATTA CTCTAATGGTGGTATCGAGAATAAA
 GACGGCGAAGTAATATCTAACTATGCTAAACTTGGTGACAATGTA AAAAGGTTGCAAGGT
 GTACAGTTTAAAACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTG
 ACAACAGTTGAAGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGGTGTGAGTCTA
 CCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAAAAAGTAATGTG
 AGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAAACATTACCAAAGCTTATGCT
 GTACCGTTTGTGTGGAATTAACAGTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAA
 ATTAATATTTACCTTAAAAACGTTGTAACCTGATGAACCAAAAACAGATAAAGATGTTAAA
 AAATTAGGTGACGACGATGACAGGTTATACGATTGGTGAAGAATTCAAATGGTTCTTGAAA
 TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA CTGATAAATTTGCA
 GATGGCTTGACTTAATACTGTTGGAAAAATCAAGATTGGTTGAAAAACACTGAATAGA
 GATGAGCACTACACTATTGATGAACCAACAGTTGATAACCAAAAATACATTA AAAAATTACG
 TTTAAACAGAGAAATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCCTGTTAAA
 AATCAAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAATT
 CCAGTTGCTCAACTATTAATGAAAAAGCAGTTTAGGAAAAAGCAATGAAAAACTTTT
 GAACCTCAATATGACCATACTCCTGATAAAGCTGACAATCCAAAACCACTAATCTCCTCA
 AGAAAACAGAAAGTTCATCTGGTGGGAAACGATTTGTAAGAAAGACTCAACAGAAAACA
 CAAACACTAGGTGGTCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGG
 ACAGATGCTCTTATTAAAGCGAATACTAATAAAAACTATAATGCTGGAGAAGCTGTTACT
 GGGCAACCAATCAAAATGAAATCACATACAGACGGTACGTTTGGATTAAAGGTTTGGCT
 TATGCAAGTTGATGCGAATGACAGGGTACAGCAGTAACTTACA AATTTAAAGAAACAAAA
 GCACCAGAAGGTTATGTAATCCCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCT
 TATAATACAAAACCAACTGACATCACGGTTGATAGTCTGATGCAACCACTGATACAATT
 AAAACAACAAAACCTCTTCAATCCCTAATACTGGTGGTATGCTGACCGCTATCTTTGTC
 GCTATCGGTGCTGCGGTGATGGCTTTTGTGTTAAGGGGATGAAGCGTCTACAAAAGAT
 AAC

SEQ ID NO. 8702
 STRAIN 090
 GCAGAAGTGTCA CAAGAACGCCCGCGAAAAC
 AGCAGTAAATATCTATAAATTA CAAGCTGATAGTTATAAATCGGAAATTA
 CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTA AAAAGGTTTGCAGGTTTACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAAGCAGCAGATGCAAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGA
 TTCAAAAGTAATGTGAGATAC TTGTAATGTAAGAAGATTTAAAGAATTAC
 CTTCAAACTTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATFACCA
 GTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAAATTAATATTTACCC
 TAAAAACGTTGTAACCTGATGAACCAAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGACGATGACGTTTATACGATTGGTGAAGAATTCAAATGGTTCT
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAAT
 TACTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
 AGATTGGTTGCAAAAACCTGAATAGAGATGAGCACTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTA AAAAATTCGTTTAAACCCAGAGAA
 ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGG
 GAAATCCAGTTGCATCAACTATTAAATGAAAAAGCAGTTT TAGGAAAAAGC
 AATTGAAAATACTTTTGAACCTTCAATATGACCCATACTCCTGATAAAGCTG
 ACAATCCAAAACCATCTAACTCCTCAAGAAAACAGAAAGTTTCACTAGGT
 GGGAAACGATTTGTAAGAAAGACTCAACAGAAAACCAAACTAGGTGG
 TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
 ATGCTCTTATTAAGCGAATACTAATAAAAACTATAATGCTGGAGAAGCT
 GTTACTGGGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGA
 GATTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGTACAGCAG
 TAACCTACA AATTTAAAGAAAACAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAAAAACATCTTATAATACAAAAC
 AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTA AAA
 ACAACAAACGCTCTTCA

SEQ ID NO. 8703
 STRAIN A909
 GCAGAAGTGTCA CAAGAACGCCCGCGAA
 AACCAACAGTAAATATCTATAAATTA CAAGCTGATAGTTATAAATCGGAAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAAACCTTGGTGACAATGTA AAAAGGTTTGCAGGTTGACAGTTTAA
 ACCTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAAGCAGCAGATGCAAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTCAGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCT
 GGAATCAAAAAGTAAATGTGAGATACTTGTATGTAGAAGATTTAAAGAAAT
 CACCTTCAAAACATTA CCAAAGCTTATGCTGTACCGTTTGTGTTGGAATTA
 CCAGTTGCTAACTCTACAGGTACAGGTTTCCCTTCTGAAATTAATATTTA
 CCCTAAaAACGTTGTAACCTGATGAACCAAAAACAGATAAAGATGTTAAAA
 AATTAGGTCAGGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGG
 TTCTTGAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGA
 AATTA CTGATAAATTTGCAGATGGCTTGACTTATAAATCTGTTGAAAAA
 TCAAGATTGGTTGCAAAAACCTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAAATACATTA AAAAATTCGTTTAAACCGA

Table 87: Comparative Sequences relating to SAG0645

GAAATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCTTGTAAAA
ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
TTGGAAATCCAGTTGTCATCAACTATTAATGAAAAAGCAGTTTtagGAAA
AGCAATTTGAAAACTTTTGAACCTCAATATGACCATACTCCTGATAAAG
CTGACAAATCCAAAACCATCTAATCTCCAAGAAAACCCAGAAGTTCATACT
GGTGGAAAACGATTTGTAAGAAAAGACTCAACAGAAAACAAAACACTAGG
TGGTCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAAATGGA
CAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
GCTGTACTGGGCAACCAATCAAATGAAATCACATACAGACGGTACGTT
TGAGATTAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAG
CAGTAACTTACAAATTAAGAAAACAAAAGCACCAGAAGGTTATGTAATC
CCTGATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAA
ACCAACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTA
AAAACAACA

SEQ ID NO. 8704

STRAIN 18RS21

GCAGAAGTGTCAAGAACGCCAGCGAAAAC
AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
CTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTAT
GCTAAACTTGGTGACAATGTAAGAGGTTTGCAAGGTGTACAGTTTAAACG
TTATAAAGTCAAGACGGATATTTCTGTTGATGAATGAAAAAATTGACAA
CAGTTGAAGCAGCAGATGCAAAAAGTTGGAACGATTCCTGAAGAAGGTGTC
AGTCTACCTCAAAAAAATAAGTCTCAAGGTTTGGTCGTGATGCTCTGGA
TTCAAAAAGTAAATGTGAGATACTTGTATGTAGAAGATTTAAAGAAATTCAC
CTTCAACATTACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACCA
GTTGCTAAGTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCC
TAAAAAGCTTGAAGTATGAAACCAAAAACAGATAAAGATGTTAAATAAT
TAGGTCAGACCGATGCAGGTTATACGATTGGTGAAGAATCAAATGGTTC
TTGAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAT
TACTGATAAATTTGCAGATGGCTTACTTATAAATCTGTTGGAAAAATCA
AGATTGGTTGAAAAACACTGAATAGAGATGAGCCTACACTATTGATGAA
CCAAAGTTGATAACCAAAAATACATTAATAAATTAAGTTTAAACAGAGAA
ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCCTGTTAAATACT
AAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTTC
GAAATTCAGTTGCATCAACTATTAAATGAAAAAGCAGTTTtagGAAAAGC
AATGAAAAATACTTTTGAACCTTCAATATGACCACTACTCCTGATAAGCTG
ACAATCCAAAACCATCTAATCTCCAAGAAAACCCAGAAGTTCATACTGGT
GGGAAACGATTTGTAAGAAAAGACTCAACAGAAAACAAAACACTAGTGG
TGCTGAGTTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAG
ATGCTCTTATAAAGCGAATACTAATAAATACTATATTGCTGGAGAAGCT
GTTACTGGGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGA
GATTAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAGCAG
TACTTACAAATTAAGAAAACAAAAGCACCAGAAGGTTATGTAATCCCT
GATAAAGAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAAC
AACTGACATCACGGTTGATAGTGTGATGCAACACCTGATACAATTA AAA
ACAACAACGTCCTTCA

SEQ ID NO. 8705

STRAIN M732

GCAGAAGTGTCAAGAACGCCAGCGAAAACAACAGT
AAATATCTATAAATTAACAAGCTGATAGTTATAAATCGGAAATTAAGTTCTA
ATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGCTAAA
CTTGGTGACAATGTAAGAGGTTTGCAAGGTGTACAGTTTAAACGTTATAA
AGTCAAGACGGATATTTCTGTTGATGAATGAAAAAATGACAACAGTGTG
AAGCAGCAGATGCAAAAGTTGGAACGATTCCTGAAGAAGGTGTGAGTCTA
CCTCAAAAAACTAATGCTCAAGGTTTGGTCGTGATGCTCTGGATTCAAA
AAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAA
ACATTAACCAAGCTTATGCTGTACCGTTTGTGTTGGAATTACAGTTGCT
AAGTCTACAGGTACAGGTTTCTTTCTGAAATTAATATTACCCTAAAAA
CGTTGTAAGTATGAAACCAAAAACAGATAAAGATGTTAAAAAATTAGGTC
AGGACGATGACAGTTATACGATTTGGTGAAGAATCAAATGGTTCTTGAAA
TCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTTGAAATTAAGTGA
TAAATTTGAGATGGCTTACTTATAAATCTGTTGGAAAAATCAAGATTG
GTTGCAAAAACACTGAATAGAGATGAGCCTACACTATTGATGAACCAACA
GTTGATAACCAAAATACATTAATAAATTAAGTTTAAACAGAGAAATTAAG
AGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAATAATCAAGATG
CTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAAT
CCAGTTGCATCAACTATTAATGAAAAGCAGTTTtagGAAAAGCAATTTGA
AAATACTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGCAATC
CAAAAACATCTAATCTCCAAGAAAACCCAGAAGTTCATACTGGTGGGAAA
CGATTTGTAAGAAAAGACTCAACAGAAAACAAAACACTAGGTTGGTCTGA
GTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAATGGACAGATGCTC
TTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACT
GGGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGGATTAAG
AGGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACTT
ACAAATTAAGAAAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAAA
GAAATCGAGTTTACAGTATCACAAACATCTTATAATACAAAACCACTGA
CATCACGGTTGATAGTGTGATGCAACACCTGATACAATTA AAAACAACA
AACGTCCTTCA

SEQ ID NO. 8706

STRAIN COHI

Table 87: Comparative Sequences relating to SAG0645

GCAGAAGTGTACAAGAACGCCAGCGAAAAC
 AGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 CTThTAATGGTGGTATCGAGAAATAAGACGGCGAAGTAATATCTAACTAT
 GCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTTGACAGTTTAAACG
 TTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 CAGTTGAGCAGCAGATGCAAAAAGTTGGAACGATTCTTGAAGAAGGTGTC
 AGTCTACCTCAAAAACTAATGCTCAAGGTTTGGTCTGTCGATGCTCTGGA
 TTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTAC
 CTTCAAAATACCAAAAGCTTATGCTGTACCCTTGTGTTGGAATTACCA
 GTTGCTAACTCFACAGGTACAGGTTTCTCTTCTGAAATTAATATTACCC
 TAAAAAGCTTGAATGATGAACCAAAAACAGATAAAGATGTTAAAAAAT
 TAGGTGAGGACGATGACAGGTTATACGATTGGTGAAGAATTCAAATGGTTC
 TTGAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAAAT
 TACTGATAAATTTGAGATGGCTTGACTTATAAATCTGTTGGAAAAATCA
 AGATTGGTTCGAAAACTGAATAGAGATGAGCCTACACTATTGATGAA
 CCAACAGTTGATAACCAAAATACATTAATAAATACGTTTAAACAGAGAA
 ATTTAAAGAAATGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATC
 AAGATGCTCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCTTTTGG
 GAAATCCAGTTGCATCAACTATTAATGAAAAGCAGTTTTAGGAAAAGC
 AATTGAAAAATCTTTGAACTTCAATATGACCATACTCCTGATAAAGCTG
 ACAATCCAAAACCACTTAATCCTCCAAGAAAACCGAAGTTCACTACTGGT
 GGGAAAACGATTTGTAAGAAAGACTCAACAGAAAACAAAACACTAGGTTGG
 TGTGAGTTTGGATTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAG
 ATGCTCTTATAAAGCGAATACTAATAAAAACTATATTGCTGGAGAACT
 GTTACTGGGCAACCAATCAAATGAAATCAATAACAGCGGTACGTTTGA
 GATTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGTACAGCAG
 TAACTTACAATTAAGAAACAAAAGCACCAGAAGGTTATGTAATCCCT
 GATAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAAAC
 AACTGACATACGGTTGATAGTGTGATGCAACACCTGATACAAATAAAA
 ACAACAAACGTCCTTCA

SEQ ID NO. 8707

STRAIN M781

GCAGAAGTGTACAAGAACGCCAGCGAAAACAG
 CAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTA
 TCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAACTATGC
 TAAACTTGGTGACAATGTAAAGGTTTGCAGGTTGACAGTTTAAACGTT
 ATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGACAA
 GTTGAAGCAGCAGATGCAAAAAGTTGGAACGATTCTTGAAGAAGGTGTG
 TCTACCTCAAAAACTAATGCTCAAGGTTTGGTCTGTCGATGCTCTGGATT
 CAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTACCT
 TCAACATTAACCAAGCTTATGCTGTACCCTTGTGTTGGAATTAACAGT
 TGCTAACTCTACAGGTACAGGTTTCTCTTCTGAAATTAATATTTACCTA
 AAAACGTTGTAACCTGATGAACCAAAAACAGATAAAGATGTTAAAAAATTA
 GGTGAGGACGATGCAAGGTTATACGATTGGTGAAGAATTCAAATGGTTCCT
 GAAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAATTTGAAATTA
 CTGATAAATTTGCAAGATGGCTTGAATATAAATCTGTTGAAAAAATCAAG
 ATTTGGTTCGAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACC
 AACAGTTGATAACCAAAATACATTAATAAATACGTTTAAACAGAGAAAT
 TTAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAAATCAA
 GATGCTCTTATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAA
 AATTCCAGTTGCATCAACTATTAATGAAAAGCAGTTTTAGGAAAAGCAA
 TTGAAAATACCTTTTGAACCTTCAATATGACCATACTCCTGATAAAGCTGAC
 AATCCAAAACCACTTAATCCTCCAAGAAAACCGAAGTTCACTACTGGTGG
 GAAAACGATTTGTAAGAAAGACTCAACAGAAAACAAAACACTAGGTGGTG
 CTGAGTTTGAATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGAT
 GCTCTTATAAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGT
 TACTGGGCAACCAATCAAATTTGAAATCACATAACAGCGGTACGTTTGGAGA
 TTAAGGTTTGGCTTATGCAAGTTGATGCGAATGACAGGGTATGATGTAATCCCTGA
 ACTTACAATTAAGAAACAAAAGCAACCGAAGGTTATGTAATCCCTGA
 TAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATACAAAACCAA
 CTGACATACGGTTGATAGTGTGATGCAACACCTGATACAAATAAAAAC
 AACAAACGT

SEQ ID NO. 8708

STRAIN CJB110

GCAGAAGTGTACAAGAACGCCAGCGAA
 AACAGCAGTAAATATCTATAAATTACAAGCTGATAGTTATAAATGGAA
 TTACTTCTAATGGTGGTATCGAGAATAAAGACGGCGAAGTAATATCTAAC
 TATGCTAAACTTGGTGACAATGTAAAGGTTTGCAGGTTGACAGTTTAA
 ACGTTATAAAGTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATTGA
 CAACAGTTGAGCAGCAGATGCAAAAAGTTGGAACGATTCTTGAAGAAGGT
 GTGCTTACCTCAAAAACTAATGCTCAAGGTTTGGTCTGTCGATGCTCT
 GGATTCAAAAAGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATT
 CACCTTCAAAATACCAAAAGCTTATGCTGTACCCTTGTGTTGGAATTA
 CAGTTGCTAACTCTACAGGTACAGGTTTCTCTTCTGAAATTAATATTA
 CCTAAAAACGTTGTAACCTGATGAACCAAAAACAGATAAAGATGTTAAAA
 AATTAGGTGAGGACGATGCAAGTTTATACGATTGGTGAAGAATTCAAATGG
 TCTTGAATCTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTGAA
 AATTACTGATAAATTTGAGATGGCTTGAATATAAATCTGTTGAAAAA
 TCAAGATTGGTTGAAAAACACTGAATAGAGATGAGCACTACACTATTGAT
 GAACCAACAGTTGATAACCAAAATACATTAATAAATACGTTTAAACAGAA
 GAAATTTAAAGAAATTTGCTGAGCTACTTAAAGGAATGACCCCTGTTAAAA

Table 87: Comparative Sequences relating to SAG0645

ATCAAGATGCTCTTGATAAAGCTACTGCAAATACAGATGATGCGGCATTT
TTGGAAATCCAGTTGCATCAACTATTAATGAAAAGCAGTTT TAGGAAA
AGCAATTGAAAATACTTTTGAACCTCAATATGACCATACTCCTGATAAAG
CTGCAATcCAAACCATCTAATCCTCCAAAGAAAACAGAGTTCACTACT
GGTGGAAACGATTTGTAAAGAAAGACTCAACAGAAAACAAAACACTAGG
TGGTGTGAGTTTGGATTGGCTTCTGATGGGACAGCAGTAAAATGGA
CAGATGCTCTTATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAA
GCTGTTACTGGGCAACCAATCAAAATGAAATCACATACAGACGGTACGTT
TGAGATTAAGGTTTGGCTTATGCAGTTGATGCGAATGCAGAGGGTACAG
CAGTAACCTTACAANTTAAAAGAAAACAAAAGCACCAGAAGGTTATGTAATC
CCTGATAAAGAAATCGAGTTTACAGTATCAAAACATCTTATAATCCAAA
ACCAACTGACATCAGGTTGATAGTGCTGATGCAACACCTGATACAATTA
AAAAACAACAAACGTCCTTCA

SEQ ID NO. 8709
STRAIN JM9130013

GCAGAAGTGTCAAGAACGCCAGCGAAAACAGCAGTA
AATATCTATAAATTACAAGCTGATAGTTATAAATCGGAAATTAAGTCTAA
TGGTGGTATCGAGAAATAAGACGGCGAAGTAAATCTAACTATGCTAAAC
TTGGTGCAATGTAAAGGTTTGCAGGTTGATCAGTTTAAACGTTATAAAA
GTCAAGACGGATATTTCTGTTGATGAATTGAAAAAATGCAACAGTTGA
AGCAGCAGATGCAAAAGTTGGAACGATTCTTGAAGAAGTGTGAGTCTAC
CTCAAAAACTAATGCTCAAGGTTTGGTCTGATGCTCTGGATTCAAAA
AGTAATGTGAGATACTTGTATGTAGAAGATTTAAAGAATTCACCTTCAAA
CATTACCAAAGCTTATGCTGTACCGTTTGTGTTGGAATACAGTTGCTA
ACTTACAGGTACAGGTTTCCCTTCTGAAATTAATATTACCTAAAAAC
GTTGTAAGTATGAAACAAAACAGATAAAGATGTTAAAAAATTAGGTCA
GGACGATGCAAGTTATACGATTTGGTGAAGAATCAAAATGGTTCTTGAAAT
CTACAATCCCTGCCAATTTAGGTGACTATGAAAAAATTTGAAATTAAGTAT
AAATTTGAGATGGCTTGAATATAAATCTGTTGAAAAAATCAAGATTTGG
TTGAAAAACACTGAATAGAGATGAGCACTACACTATTGATGAACCAACAG
TTGATAACCAAAATACATTAATAAATACGTTTAAACAGAGAAATTTAAA
GAAATTTGCTGAGCTACTTAAAGGAATGACCTTGTATAAATCAAGATGC
TCTTGATAAAGCTACTGCAAAATACAGATGATGCGGCATTTTGGAAAATTC
CAGTTGCATCAACTATTAATGAAAAGCAGTTT TAGGAAAAGCAATTTGAA
AATACTTTGAACTTCAATATGACCATACTCTGATAAAGCTGACAAATCC
AAAACCATCTAATcCTcCAAGAAAACCGAAGTTCATACTGGTGGGAAAC
GATTTGTAAGAAAAGACTCAACAGAAAACAAAACACTAGGTTGGTGTGAG
TTTGATTTGTTGGCTTCTGATGGGACAGCAGTAAAATGGACAGATGCTCT
TATTAAGCGAATACTAATAAAAACTATATTGCTGGAGAAGCTGTTACTG
GGCAACCAATCAAATGAAATCACATACAGACGGTACGTTTGGAGATTAAA
GGTTTGGCTTATGCAAGTTGATGCGAATGCAGAGGGTACAGCAGTAACCTTA
CAAATTAAGAAAACAAAAGCACCAGAAGGTTATGTAATCCCTGATAAAG
AAATCGAGTTTACAGTATCAAAACATCTTATAATAACAAAACCAACTGAC
ATCAGGTTGATAGTGCTGATGCAACACCTGATACAATTAATAAACAACAA
ACGTCCTTCA

PRETTY of: /biotmp/msa123961.2{*} April 30, 2003 07:17 ..

msa123961.2{80_2603} 1 atgaaattat cgaagaagtt attgttttctg gctgctgttt taacaatggt 50
msa123961.2{80_A909}
msa123961.2{80_M732}
msa123961.2{80_090}
msa123961.2{80_COH1}
msa123961.2{80_M781}
msa123961.2{801_JM9130013}
msa123961.2{80_18RS21}
msa123961.2{80h_CJB110}
Consensus

msa123961.2{80_2603} 51 ggcgggggtca actggtgaac cagtagctca gtttgcgact ggaatgagta 100
msa123961.2{80_A909}
msa123961.2{80_M732}
msa123961.2{80_090}
msa123961.2{80_COH1}
msa123961.2{80_M781}
msa123961.2{801_JM9130013}
msa123961.2{80_18RS21}
msa123961.2{80h_CJB110}
Consensus

msa123961.2{80_2603} 101 ttgtaagagc tGCAGAAGTG TCACAAGAAC GCCCAGCGAA AACAAcAGTA 150
msa123961.2{80_A909}
msa123961.2{80_M732}
msa123961.2{80_090}
msa123961.2{80_COH1}
msa123961.2{80_M781}
msa123961.2{801_JM9130013}
msa123961.2{80_18RS21}
Consensus

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80h_CJB110}	-----	-GCAGAAGTG	TCACAAGAAC	GCCCAGCGAA	AACAgCAGTA
Consensus	-----	*****	*****	*****	*****
	151				200
msa123961.2{80_2603}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_A909}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_M732}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_090}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_COH1}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_M781}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{801_JM9130013}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80_18RS21}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
msa123961.2{80h_CJB110}	AATATCTATA	AATTACAAGC	TGATAGTTAT	AAATcGGAAA	TTACTTcTAA
Consensus	*****	*****	*****	*****	*****
	201				250
msa123961.2{80_2603}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_A909}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_M732}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_090}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_COH1}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_M781}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{801_JM9130013}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80_18RS21}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
msa123961.2{80h_CJB110}	TGGTGGTATC	GAGAATAAAG	ACGGCGAAGT	AATATCTAAC	TATGCTAAAC
Consensus	*****	*****	*****	*****	*****
	251				300
msa123961.2{80_2603}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_A909}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_M732}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_090}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_COH1}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_M781}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{801_JM9130013}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80_18RS21}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
msa123961.2{80h_CJB110}	TTGGTGACAA	TGTA AAAAGGT	TTGCAAGGTG	TACAGTTTAA	ACGTTATAAA
Consensus	*****	*****	*****	*****	*****
	301				350
msa123961.2{80_2603}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_A909}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_M732}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_090}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_COH1}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_M781}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{801_JM9130013}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80_18RS21}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
msa123961.2{80h_CJB110}	GTCAAGACGG	ATATTTCTGT	TGATGAATTG	AAAAAATTGA	CAACAGTTGA
Consensus	*****	*****	*****	*****	*****
	351				400
msa123961.2{80_2603}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_A909}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_M732}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_090}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_COH1}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_M781}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{801_JM9130013}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80_18RS21}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
msa123961.2{80h_CJB110}	AGCAGCAGAT	GCAAAAAGTTG	GAACGATTCT	TGAAGAAGGT	GTCAGTCTAC
Consensus	*****	*****	*****	*****	*****
	401				450
msa123961.2{80_2603}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_A909}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_M732}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_090}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_COH1}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_M781}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{801_JM9130013}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80_18RS21}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
msa123961.2{80h_CJB110}	CTCAAAAAAC	TAATGCTCAA	GGTTTGGTCG	TCGATGCTCT	GGATTCAAAA
Consensus	*****	*****	*****	*****	*****
	451				500
msa123961.2{80_2603}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_A909}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_M732}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_090}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_COH1}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80_M781}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{801_JM9130013}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_18RS21}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
msa123961.2{80h_CJB110}	AGTAATGTGA	GATACTTGTA	TGTAGAAGAT	TTAAAGAATT	CACCTTCAAA
Consensus	*****	*****	*****	*****	*****
501					
msa123961.2{80_2603}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_A909}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M732}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_090}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_COH1}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_M781}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{801_JM9130013}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80_18RS21}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
msa123961.2{80h_CJB110}	CATTACCAA	GCTTATGCTG	TACCGTTTGT	GTGGAATTA	CCAGTTGCTA
Consensus	*****	*****	*****	*****	*****
551					
msa123961.2{80_2603}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_A909}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M732}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_090}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_COH1}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_M781}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{801_JM9130013}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80_18RS21}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
msa123961.2{80h_CJB110}	ACTCTACAGG	TACAGGTTTC	CTTTCTGAAA	TTAATATTTA	CCCTAAAAAC
Consensus	*****	*****	*****	*****	*****
601					
msa123961.2{80_2603}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_A909}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_M732}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_090}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_COH1}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_M781}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{801_JM9130013}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80_18RS21}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
msa123961.2{80h_CJB110}	GTGTAACTG	ATGAACCAA	AACAGATAAA	GATGTTAAAa	AATTAGGTCA
Consensus	*****	*****	*****	*****	*****
651					
msa123961.2{80_2603}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_A909}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_M732}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_090}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_COH1}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_M781}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{801_JM9130013}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80_18RS21}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
msa123961.2{80h_CJB110}	GGACGATGCA	GGTTATACGA	TTGGTGAAGA	ATTCAAATGG	TTCTTGAAT
Consensus	*****	*****	*****	*****	*****
701					
msa123961.2{80_2603}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_A909}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M732}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_090}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_COH1}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_M781}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{801_JM9130013}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80_18RS21}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
msa123961.2{80h_CJB110}	CTACAATCCC	TGCCAATTTA	GGTGACTATG	AAAAATTTGA	AATTACTGAT
Consensus	*****	*****	*****	*****	*****
751					
msa123961.2{80_2603}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_A909}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M732}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_090}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_COH1}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_M781}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{801_JM9130013}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80_18RS21}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
msa123961.2{80h_CJB110}	AAATTTGCAG	ATGGCTTGAC	TTATAAATCT	GTTGGAAAAA	TCAAGATTGG
Consensus	*****	*****	*****	*****	*****
801					
msa123961.2{80_2603}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_A909}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_M732}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_090}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_COH1}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG
msa123961.2{80_M781}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACATTGAT	GAACCAACAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{801_JM9130013}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80_18RS21}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
msa123961.2{80h_CJB110}	TTCGAAAACA	CTGAATAGAG	ATGAGCACTA	CACTATTGAT	GAACCAACAG
Consensus	*****	*****	*****	*****	*****
	851				900
msa123961.2{80_2603}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_A909}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M732}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_090}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_COH1}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_M781}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{801_JM9130013}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80_18RS21}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
msa123961.2{80h_CJB110}	TTGATAACCA	AAATACATTA	AAAATTACGT	TTAAACCAGA	GAAATTTAAA
Consensus	*****	*****	*****	*****	*****
	901				950
msa123961.2{80_2603}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_A909}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_M732}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_090}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_COH1}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_M781}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{801_JM9130013}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80_18RS21}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
msa123961.2{80h_CJB110}	GAAATTGCTG	AGCTACTTAA	AGGAATGACC	CTTGTAAAA	ATCAAGATGC
Consensus	*****	*****	*****	*****	*****
	951				1000
msa123961.2{80_2603}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_A909}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M732}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_090}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_COH1}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_M781}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{801_JM9130013}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80_18RS21}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
msa123961.2{80h_CJB110}	TCTTGATAAA	GCTACTGCAA	ATACAGATGA	TGCGGCATT	TTGGAAATTC
Consensus	*****	*****	*****	*****	*****
	1001				1050
msa123961.2{80_2603}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80_A909}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80_M732}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80_090}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80_COH1}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80_M781}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{801_JM9130013}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80_18RS21}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
msa123961.2{80h_CJB110}	CAGTTGCATC	AACTATTAAT	GAAAAGCAG	TTTTAGGAAA	AGCAAITGAA
Consensus	*****	*****	*****	*****	*****
	1051				1100
msa123961.2{80_2603}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_A909}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M732}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_090}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_COH1}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_M781}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{801_JM9130013}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80_18RS21}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
msa123961.2{80h_CJB110}	AATACFTTTG	AACFTCAATA	TGACCATACT	CCTGATAAAG	CTGACAATCC
Consensus	*****	*****	*****	*****	*****
	1101				1150
msa123961.2{80_2603}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_A909}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M732}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_090}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_COH1}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_M781}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{801_JM9130013}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80_18RS21}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
msa123961.2{80h_CJB110}	AAAACCATCT	AATCCTCCAA	GAAAACCAGA	AGTTCATACT	GGTGGGAAAC
Consensus	*****	*****	*****	*****	*****
	1151				1200
msa123961.2{80_2603}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_A909}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_M732}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_090}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG
msa123961.2{80_COH1}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACACTAGG	TGGTGCTGAG

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_M781}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACTACTAGG	TGGTGCCTGAG
msa123961.2{801_JM9130013}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACTACTAGG	TGGTGCCTGAG
msa123961.2{80_18RS21}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACTACTAGG	TGGTGCCTGAG
msa123961.2{80h_CJB110}	GATTTGTAAA	GAAAGACTCA	ACAGAAACAC	AAACTACTAGG	TGGTGCCTGAG
Consensus	*****	*****	*****	*****	*****
	1201				1250
msa123961.2{80_2603}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80_A909}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80_M732}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80_090}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80_COH1}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80_M781}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{801_JM9130013}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80_18RS21}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
msa123961.2{80h_CJB110}	TTTGATTTGT	TGGCTTCTGA	TGGGACAGCA	GTAATAATGGA	CAGATGCTCT
Consensus	*****	*****	*****	*****	*****
	1251				1300
msa123961.2{80_2603}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_A909}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M732}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_090}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_COH1}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_M781}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{801_JM9130013}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80_18RS21}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
msa123961.2{80h_CJB110}	TATTAAGCG	AATACTAATA	AAAACATATAT	TGCTGGAGAA	GCTGTTACTG
Consensus	*****	*****	*****	*****	*****
	1301				1350
msa123961.2{80_2603}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_A909}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M732}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_090}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_COH1}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_M781}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{801_JM9130013}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80_18RS21}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
msa123961.2{80h_CJB110}	GGCAACCAAT	CAAATTGAAA	TCACATACAG	ACGGTACGTT	TGAGATTAAA
Consensus	*****	*****	*****	*****	*****
	1351				1400
msa123961.2{80_2603}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_A909}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M732}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_090}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_COH1}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_M781}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{801_JM9130013}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80_18RS21}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
msa123961.2{80h_CJB110}	GGTTTGGCTT	ATGCAGTTGA	TGCCAATGCA	GAGGGTACAG	CAGTAACCTA
Consensus	*****	*****	*****	*****	*****
	1401				1450
msa123961.2{80_2603}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_A909}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M732}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_090}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_COH1}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_M781}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{801_JM9130013}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80_18RS21}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
msa123961.2{80h_CJB110}	CAAATTAATA	GAAACAAAAG	CACCAGAAGG	TTATGTAATC	CCTGATAAAG
Consensus	*****	*****	*****	*****	*****
	1451				1500
msa123961.2{80_2603}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_A909}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M732}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_090}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_COH1}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_M781}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{801_JM9130013}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80_18RS21}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
msa123961.2{80h_CJB110}	AAATCGAGTT	TACAGTATCA	CAAACATCTT	ATAATaCAAA	ACCAACTGAC
Consensus	*****	*****	*****	*****	*****
	1501				1550
msa123961.2{80_2603}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_A909}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M732}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_090}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA

Table 87: Comparative Sequences relating to SAG0645

msa123961.2{80_COH1}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_M781}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{801_JM9130013}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80_18RS21}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
msa123961.2{80h_CJB110}	ATCACGGTTG	ATAGTGCTGA	TGCAACACCT	GATACAATTA	AAAACAACAA
Consensus	*****	*****	*****	*****	*****
	1551				1600
msa123961.2{80_2603}	acgtccttca	atccctaata	ctgggtggtat	tggtacggct	atctttgtcg
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_090}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_COH1}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_M781}	acgt	-----	-----	-----	-----
msa123961.2{801_JM9130013}	acgtccttca	-----	-----	-----	-----
msa123961.2{80_18RS21}	acgtccttca	-----	-----	-----	-----
msa123961.2{80h_CJB110}	acgtccttca	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
	1601				1650
msa123961.2{80_2603}	ctatcgggtgc	tcgggtgatg	gcttttgcgtg	ttaaggggat	gaagcgtcgt
msa123961.2{80_A909}	-----	-----	-----	-----	-----
msa123961.2{80_M732}	-----	-----	-----	-----	-----
msa123961.2{80_090}	-----	-----	-----	-----	-----
msa123961.2{80_COH1}	-----	-----	-----	-----	-----
msa123961.2{80_M781}	-----	-----	-----	-----	-----
msa123961.2{801_JM9130013}	-----	-----	-----	-----	-----
msa123961.2{80_18RS21}	-----	-----	-----	-----	-----
msa123961.2{80h_CJB110}	-----	-----	-----	-----	-----
Consensus	-----	-----	-----	-----	-----
	1651				1662
msa123961.2{80_2603}	acaaaagata	ac			
msa123961.2{80_A909}	-----	-----			
msa123961.2{80_M732}	-----	-----			
msa123961.2{80_090}	-----	-----			
msa123961.2{80_COH1}	-----	-----			
msa123961.2{80_M781}	-----	-----			
msa123961.2{801_JM9130013}	-----	-----			
msa123961.2{80_18RS21}	-----	-----			
msa123961.2{80h_CJB110}	-----	-----			
Consensus	-----	-----			

SEQ ID NO. 8710

STRAIN 2603 frame: 1

MKLSKLLFSAAVLTVMAGSTVEPVAQFATGMSIVRAAEVSOERPAKTTVNIYKLQADSY
KSEITSNNGIENKDGSEVSNYAKLGDNVKGLQGVQFKRYKVKTDIISVDELKCLTVEAAD
AKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLYVEDLKNSPSNITKAYAVPFVLEL
PVANSTGTGFLSEINIYPKNVVTDEPKTKDKVVKLGQDDAGYTIIEEFKWFLLKSTIPANL
GDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHYTIDEPTVDNQNTLKITFKPEKFK
EIAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVASTINEKAVLGKAIENTFELQYDHT
PDKADNPKPSNPPRKPPEVHTGGKRFVKKDSTETQTLGGAEPDLLASDGTAVKWTDALIKA
NTNKNYIAGEAVTGPQIKLKSHTDGTFEIKGLAYAVDANAEGTAVTYKPKETKAPEGYVI
PDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNKRPSIPNTGGIGTAIFVAIGAAMV
AFAVKGMKRRTKDN

SEQ ID NO. 8711

STRAIN 090 frame: 1

AEVSOERPAKTTVNIYKLQADSYKSEITSNNGIENKDGSEVSNYAKLGDNVKGLQGVQFK
RYKVKTDIISVDELKCLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELIPVANSTGTGFLSEINIYPKNVVTDEPKTKDKVVKLGQ
DDAGYTIIEEFKWFLLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGPQIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKPKETKAPEGYVIVPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8712

STRAIN 18RS21 frame: 1

AEVSOERPAKTTVNIYKLQADSYKSEITSNNGIENKDGSEVSNYAKLGDNVKGLQGVQFK
RYKVKTDIISVDELKCLTVEAADAKVGTILEEGVSLPQKTNAQGLVVDALDSKSNVRYLY
VEDLKNSPSNITKAYAVPFVLELIPVANSTGTGFLSEINIYPKNVVTDEPKTKDKVVKLGQ
DDAGYTIIEEFKWFLLKSTIPANLGDYKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKITFKPEKFKIEAELLKGMTLVKNQDALDKATANTDDAAFLIEIPVAS
TINEKAVLGKAIENTFELQYDHTPDKADNPKPSNPPRKPPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGPQIKLKSHTDGTFEIKGLAYAVD
ANAEGTAVTYKPKETKAPEGYVIVPDKEIEFTVSQTSYNTKPTDITVDSADATPDTIKNNK
RPS

SEQ ID NO. 8713

STRAIN M732 frame: 1

AEVSOERPAKTTVNIYKLQADSYKSEITSNNGIENKDGSEVSNYAKLGDNVKGLQGVQFK

Table 87: Comparative Sequences relating to SAG0645

RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPLVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKI TFKPEKFKIEAELLKGM TLVKNQDALDKATANTDDAAFL EIPVAS
TINEKAVLGKAI ENT FELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIK LKSHTDGT FEIKGLAYAVD
ANABGTAVTYK LK KETKAPEGYV I PDKEIEFTVSQTSYNTKPTDI TVDSADATPDTIKNK
RPS

SEQ ID NO. 8714
STRAIN M781 frame: 1
AEVSQERPAKTA VNIYKLQADSYKSEITSNGGIENKDGEV I SNYAKLGDNVKLGQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPLVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKI TFKPEKFKIEAELLKGM TLVKNQDALDKATANTDDAAFL EIPVAS
TINEKAVLGKAI ENT FELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIK LKSHTDGT FEIKGLAYAVD
ANABGTAVTYK LK KETKAPEGYV I PDKEIEFTVSQTSYNTKPTDI TVDSADATPDTIKNK
R

SEQ ID NO. 8715
STRAIN COH1 frame: 1
AEVSQERPAKTA VNIYKLQADSYKSEITXNGGIENKDGEV I SNYAKLGDNVKLGQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPLVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKI TFKPEKFKIEAELLKGM TLVKNQDALDKATANTDDAAFL EIPVAS
TINEKAVLGKAI ENT FELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIK LKSHTDGT FEIKGLAYAVD
ANABGTAVTYK LK KETKAPEGYV I PDKEIEFTVSQTSYNTKPTDI TVDSADATPDTIKNK
RPS

SEQ ID NO. 8716
STRAIN CJB110 frame: 1
AEVSQERPAKTA VNIYKLQADSYKLEITSNGGIENKDGEV I SNYAKLGDNVKLGQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPLVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKI TFKPEKFKIEAELLKGM TLVKNQDALDKATANTDDAAFL EIPVAS
TINEKAVLGKAI ENT FELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIK LKSHTDGT FEIKGLAYAVD
ANABGTAVTYK LK KETKAPEGYV I PDKEIEFTVSQTSYNTKPTDI TVDSADATPDTIKNK
RPS

SEQ ID NO. 8717
STRAIN JM9130013 frame: 1
AEVSQERPAKTA VNIYKLQADSYKSEITSNGGIENKDGEV I SNYAKLGDNVKLGQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPLVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKI TFKPEKFKIEAELLKGM TLVKNQDALDKATANTDDAAFL EIPVAS
TINEKAVLGKAI ENT FELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIK LKSHTDGT FEIKGLAYAVD
ANABGTAVTYK LK KETKAPEGYV I PDKEIEFTVSQTSYNTKPTDI TVDSADATPDTIKNK
RPS

SEQ ID NO. 8718
STRAIN A909 frame: 1
AEVSQERPAKTTVNIYKLQADSYKSEITSNGGIENKDGEV I SNYAKLGDNVKLGQGVQFK
RYKVKTDISVDELKKLTTVEAADAKVGTILEEGVSLPQKTNAGGLVVDALDSKSNVRVLY
VEDLKNSPSNITKAYAVPFVLELPLVANSTGTGFLSEINIYPKNVVTDEPKTDKDVKKLGQ
DDAGYTI GEEFKWFLKSTIPANLGDYEFKFEITDKFADGLTYKSVGKIKIGSKTLNRDEHY
TIDEPTVDNQNTLKI TFKPEKFKIEAELLKGM TLVKNQDALDKATANTDDAAFL EIPVAS
TINEKAVLGKAI ENT FELQYDHTPDKADNPKPSNPPRKPEVHTGGKRFVKKDSTETQTLG
GAEPDLLASDGTAVKWTDALIKANTNKNYIAGEAVTGQPIK LKSHTDGT FEIKGLAYAVD
ANABGTAVTYK LK KETKAPEGYV I PDKEIEFTVSQTSYNTKPTDI TVDSADATPDTIKNK

PRETTY of: /biotmp/msa124060.2{*} April 30, 2003 07:19 ..

Table with 2 columns: sequence identifiers (e.g., msa124060.2{80_2603}) and alignment markers (1, 50, dashes, asterisks).

Table 87: Comparative Sequences relating to SAG0645

	51			100
msa124060.2{80_2603}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80_M732}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80_A909}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80_090}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80_M781}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80_COH1}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{801_JM9130013}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80_18RS21}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
msa124060.2{80h_CJB110}	NIYKIQADSY	KsEITsNGGI	ENKDGIVISN	YAKLGDNVKG
	Consensus	*****	*_*_*_*_*_*_*_*	*****
	101			150
msa124060.2{80_2603}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80_M732}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80_A909}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80_090}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80_M781}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80_COH1}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{801_JM9130013}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80_18RS21}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
msa124060.2{80h_CJB110}	VKTDISVDEL	KKLTTVEAAD	AKVGTILEEG	VSLPQKTNAQ
	Consensus	*****	*****	*****
	151			200
msa124060.2{80_2603}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80_M732}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80_A909}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80_090}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80_M781}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80_COH1}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{801_JM9130013}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80_18RS21}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
msa124060.2{80h_CJB110}	SNVRYLYVED	LKNSPSNITK	AYAVPFVLEL	PVANSTGTGF
	Consensus	*****	*****	*****
	201			250
msa124060.2{80_2603}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80_M732}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80_A909}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80_090}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80_M781}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80_COH1}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{801_JM9130013}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80_18RS21}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
msa124060.2{80h_CJB110}	VVTDEPKTDK	DVKKLGQDDA	GYYIGEEFKW	FLKSTIPANL
	Consensus	*****	***_*_*_*_*_*_*_*	*****
	251			300
msa124060.2{80_2603}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80_M732}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80_A909}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80_090}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80_M781}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80_COH1}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{801_JM9130013}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80_18RS21}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
msa124060.2{80h_CJB110}	KFADGLTYKS	VGKIKIGSKT	LNRDEHYTID	EPTVDNQNTL
	Consensus	*****	*****	*****
	301			350
msa124060.2{80_2603}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80_M732}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80_A909}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80_090}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80_M781}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80_COH1}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{801_JM9130013}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80_18RS21}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
msa124060.2{80h_CJB110}	EIAELLKGMT	LVKNQDALDK	ATANTDDAAF	LEIPVASTIN
	Consensus	*****	*****	*****
	351			400
msa124060.2{80_2603}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80_M732}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80_A909}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80_090}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80_M781}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80_COH1}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{801_JM9130013}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80_18RS21}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
msa124060.2{80h_CJB110}	NTFELQYDHT	PKADNPKPS	NPPRKPEVHT	GKRFVKKDS
	Consensus	*****	*****	*****

Table 87: Comparative Sequences relating to SAG0645

	401				450
msa124060.2{80_2603}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80_M732}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80_A909}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80_090}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80_M781}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80_COH1}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{801_JM9130013}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80_18RS21}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
msa124060.2{80h_CJB110}	FDLLASDGTA	VKWTDALIKA	NTNKNYIAGE	AVTGQPIKLL	SHTDGTFEIK
Consensus	*****	*****	*****	*****	*****
	451				500
msa124060.2{80_2603}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80_M732}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80_A909}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80_090}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80_M781}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80_COH1}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{801_JM9130013}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80_18RS21}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
msa124060.2{80h_CJB110}	GLAYAVDANA	EGTAVTYKLL	ETKAPEGYVI	PDKEIEFTVS	QTSYntKPTD
Consensus	*****	*****	*****	*****	*****
	501				550
msa124060.2{80_2603}	ITVDSADATP	DTIKNNkrps	ipntggigta	ifvaigaavm	afavkgmkrr
msa124060.2{80_M732}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_A909}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_090}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_M781}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_COH1}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{801_JM9130013}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80_18RS21}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
msa124060.2{80h_CJB110}	ITVDSADATP	DTIKNNkrps	-----	-----	-----
Consensus	*****	*****	-----	-----	-----
	551				
msa124060.2{80_2603}	tkdn				
msa124060.2{80_M732}	----				
msa124060.2{80_A909}	----				
msa124060.2{80_090}	----				
msa124060.2{80_M781}	----				
msa124060.2{80_COH1}	----				
msa124060.2{801_JM9130013}	----				
msa124060.2{80_18RS21}	----				
msa124060.2{80h_CJB110}	----				
Consensus	----				

Table 88: Comparative Sequences relating to SAG0477

SEQ ID NO. 8801

STRAIN 2603

ATGCCCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTTGTCTTAACGGAATGGCAA
AAGCGTAACCTTGAATTTTAAAAAAACGCAAGAAGATGAAGAAGAACAAAAACGTAAT
AACGAAAAATACCGCTTAGATAAAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCT
CAAAATACACTACTAAAATTAAGAAGCTTCATTTTCCAAAGATTCAAGACCTAAGATTGAA
AAGAAACGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCATTAGAACT
GCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTCCGTTTTCTACTAATCCT
TTTAGTAAGCAAAAAAANTAACAGTTAGTGGAAATCAGCATAACCTGATGATATTTTG
ATAGAGAAAAACGAAATATTCAAAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAA
GCTATTTGAACAACGTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
CAATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATGTCATATGCACAT
ACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAGGCTGATCCTGTAAATAGT
TCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAAGATAGTATTAAAGCTA
TTAATTAAGATTTAAAGGCTTTAGACCTGATTTAATAAGTGAAGATTGAGGTGATAAGT
TTAGCTGATTTCAAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAATAGT
ATTAGAATACCAATTTCTAAATTTAAGAAAGACTTCTTTTACAAACAATTAAGAAG
AACCTTAAGGAACTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACAATACC
ATTGAATCAACCTCTGTTAAAGCAGAAGATACAAAAATAAATCACTGATAAAACACAA
ACCAAAATGGTCAAGTTGCGGAAATAGTCAAGGACAAAACAATACTCAAACTAAT
CAACAGGACAACAGATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8802

STRAIN H36B

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTAATTAACGAAAAATTAACGCTTAGATA
AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
GAAACGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCA
TTAGAACCTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
GTTTTCTACTAATCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTGATAGAGAAAACGAAATTTCAA
AAAACGATTTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATGTCAT
ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
GCTGATCCTGTAAATAGTTTCAAGAGCTACCAAGCACTTCTTAACAATTA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCTT
TAGACCTGATTTAATAAGTGAAGTTCAAGGTGATAAGTTTAGCTGATTTCT
AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAATAGTAT
TAGAATACCATTTACTAAATTTAAGAAAGACTTCTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
AAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAAGTTGCGG
AAAATAGTCAAGGACAAAACAATACTCAAACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8803

STRAIN 18RS21

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAGTT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGCAA
AGAAGATGAAGAAGAACAAAAACGTAATTAACGAAAAATTAACGCTTAGATA
AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCCTCAAAATACTACT
AAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAA
GAAACGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCGCA
TTAGAACCTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTTCC
GTTTTCTACTAATCCTTTTAGTAAGCAAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTGATAGAGAAAACGAAATTTCAA
AAAACGATTTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATGTCAT
ATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAACTGGAAAAAG
GCTGATCCTGTAAATAGTTTCAAGAGCTACCAAGCACTTCTTAACAATTA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCTT
TAGACCTGATTTAATAAGTGAAGTTCAAGGTGATAAGTTTAGCTGATTTCT
AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAATAGTAT
TAGAATACCATTTACTAAATTTAAGAAAGACTTCTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
TACACAACAACAATAACCATTTGAATCAACCCCTGTTAAAGCAGAAGATAC
AAAAATAAATCAACTGATAAAACACAAACACAAAATGGTCAAGTTGCGG
AAAATAGTCAAGGACAAAACAATACTCAAACTAATCAACAAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8804

STRAIN M732

CCTAAGAAGAAATCAGATACCCAGAAAAAGAAGAG
TTGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAAACGCG
AAAGAAGATGAAGAAGAACAAAAACGTAATTAACGAAAAATTAACGCTTAGA
TAAAAGAGTAAATTAATATTTCTTCTCCTGAAGAACCCTCAAAATACTA
CTAAAAATTAAGAAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAA
AAGAAACGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAATAATCG
CATTAGAACTGCACCTATATTTGTAGTAGCATTCCTAGTCATTTAGTTT

Table 88: Comparative Sequences relating to SAG0477

CCGTTTTCTACTAACTCCTTTTAGTAAGCAAAAAACAATAACAGTTAGT
 GGAAATCAGCATAACCTGATGATAITTTGATAGAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAATTAAGATTAAAGGC
 TTTAGACCCTGATTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATT
 CTAAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTTTACAAACA
 AATTAAGAAGAACCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAAACACAACCAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8805

STRAIN COH1

CCTAAGAAGAAATCAGATACCCCGAAAAAGAAGAGTT
 GTCTTAAACGGAAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAA
 AGAAGATGAAGAAGAACAAAAACGTTAATTAACGAAAAATTACGCTTAGATA
 AAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTACT
 AAAATTAAGAAGCTTCAATTTTCAAAGATTTCAAAACCTTAAGATTGAAAA
 GAAACAGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCA
 TTAGAACTGCACCTATATTTGTAGTAGCATTCTTAGTCATTTTAGTTTCC
 GTTTTCTACTAACTCCTTTTAGTAGCAAAAAACAATAACAGTTAGTGG
 AAATCAGCATACACCTGATGATATTTGTAGAAAAAACGAATATTCAA
 AAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAA
 CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
 ATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATTGCAT
 ATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAAAG
 GCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATTA
 CCTTGATAAGGAAGATAGTATTAGCTATTAATTAAGATTAAAGGCTT
 TAGACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATTCT
 AAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGTAT
 TAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTTTACAAACAA
 TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTT
 TACACAACAACAAGTACTATTGAATCAACCCTGTGAAAGCGGAAGATAC
 AAAAAATAAATCAACTGATAAAAACACAACCAAAATGGTCAGGTTGCGG
 AAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGACAA
 CAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8806

STRAIN M781

CCTAAGAAGAAATCAGATACCCCGAAAAAGAAGAG
 TTGCTTAAACGGAAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTTAATTAACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAAATTAAGAAGCTTCAATTTTCAAAGATTTCAAAACCTTAAGATTGAA
 AAGAAACGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCG
 CATTAGAAGCTGCACCTATATTTGTAGTAGCATTCTTAGTCATTTTAGTTT
 CCGTTTCTACTAACTCCTTTTAGTAGCAAAAAACAATAACAGTTAGT
 GGAATCAGCATACACCTGATGATATTTGTAGAAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATT
 CTAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAAACACAACCAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

SEQ ID NO. 8807

STRAIN CJB110

CCTAAGAAGAAATCAGATACCCCGAAAAAGAAGAG
 TTGCTTAAACGGAAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCG
 AAAGAAGATGAAGAAGAACAAAAACGTTAATTAACGAAAAATTACGCTTAGA
 TAAAGAAGTAAATTAATATTTCTTCTCCTGAAGAACCTCAAAATACTA
 CTAAAATTAAGAAGCTTCAATTTTCAAAGATTTCAAAACCTTAAGATTGAA
 AAGAAACGAAAAAGAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCG
 CATTAGAAGCTGCACCTATATTTGTAGTAGCATTCTTAGTCATTTTAGTTT
 CCGTTTCTACTAACTCCTTTTAGTAGCAAAAAACAATAACAGTTAGT
 GGAATCAGCATACACCTGATGATATTTGTAGAAAAAACGAATATTCA
 AAAAAACGATTATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAAC
 AACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTAT
 CAATTTCCCAATAAGTTTCATATTTCAAGTTCAAGAAAAAAGATTATTGC
 ATATGCACATACAAGCAAGGATATCAGCCTGTCTTGGAACTGGAAAA
 AGGCTGATCCTGTAAATAGTTTCAGAGCTACCAAAGCACTTCTTAACAATT
 AACCTTGATAAGGAAGATAGTATTAGCTATTAAATTAAGATTAAAGGC
 TTTAGACCCTGATTTAATAAGTGAGATTGAGGTGATAAGTTTAGCTGATT
 CTAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAATAGT
 ATTAGAATACCATTTATCTAAATTTAAAGAAAGACTTCTTTTTTACAAACA
 AATTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
 TTTACACAACAACAAGTACTATTGAATCAACCCTGTGAAAGCGGAAGAT
 ACAAAAAATAAATCAACTGATAAAAACACAACCAAAATGGTCAGGTTGC
 GGAAATAGTCAAGGACAAACAATAACTCAATACTAATCAACAAGGAC
 AACAGATAGCAACAGAGCAGGCACCCACCTCAAAATGTTAAT

Table 88: Comparative Sequences relating to SAG0477

ATATGCACATACAAAGCAAGGATATCAGCCTGTCTTGAAACTGGAAAA
AGGCTGATCCTGTAAATAGTTCAGAGCTACCAAGCACTTCTTAACAATT
AACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGC
TTTAGACCTGATTTAATAAGTGAAGATTGAGTGAAGTTTAGCTGATT
CTAAAACGACACCTGACCTCCTGCTGTAGATATGCATGATGGAAATAGT
ATTAGAATACCAATTATCTAAATTTAAGAAAGACTTCCTTTTACAAACA
AATTAAGAAAGAACTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAG
TTTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGAT
ACAAAAATAAATCAACTGATAAAACACAACACAAATGGTCAGGTGCG
GGAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAGGAC
AACAGATAGCAACAGAGCAGGCACCCCAACCTCAAATGTTAAT

SEQ ID NO. 8808

STRAIN 1169NT

CCTAAGAAGAAATCAGATACCCCGAAAAAGAAGT
TGTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
AAGAAGTGAAGAAGAACAACAAACGTATTACGAAAAATTACGCTTAGAT
AAAAGAAGTAAATTAATATTTCTCTCCTGAAGAACCTCAAATACTAC
TAAATTAAGAAAGCTTCATTTTCCAAAGATTTCAAACCTAAGATTGAAA
AGAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAATACTCGC
ATTAGAATGACCTGACCTATATTATAGTAGCATTCTAGTCATTTAGTTT
CGTTTTCTACTAACTCCTTTTAGTAAGCAAAAACAATAACAGTTAGTG
GAAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAA
AAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
ACGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATC
AATTTCCCAACAAGTTTCATATTCAAGTTCAAGAAAAAAGATTATTGCA
TATGCACATACAAAGCAAGGATATCAGCCTGTCTTGGAAACTGGAAAAA
GGCTGATCCTGTAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
ACCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCT
TTAGACCTGATTTAATAAGTGAAGATTGAGGTGATAAGTTTAGCTGATT
TAAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTA
TTAGAATACCATTAATCTAAATTTAAGAAAGACTTCCTTTTACAAACAA
ATTAAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
TTACACAACAACAAGTACTATTGAATCAACCCCTGTGAAAGCGGAAGATA
CAAAAAATAAATCAACTGATAAAACACAACCCAAAATGGTCAGGTGCGG
GAAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAGGACA
ACAAAGATAGCAACAGGAGCAGGCACCCCAACCTCAAATGTTAAT

SEQ ID NO. 8809

STRAIN JM9130013

CCTAAGAAGAAATCAGATACCCCGAAAAAGAAGT
GTCTTAACGGAATGGCAAAAGCGTAACCTTGAATTTTAAAAAACGCA
AGAAGATGAAGAAGAACAACAAACGTATTACGAAAAATTACGCTTAGATA
AAAGAAGTAAATTAATATTTCTCTCCTGAAGAACCTCAAATACTACT
AAAATTAAGAAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAA
GAAACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAATACTCGCA
TTAGAATGACCTGACCTATATTGTAAGTAGCATTCTAGTCATTTAGTTT
GTTTTCTACTAACTCCTTTTAGTAAGCAAAAACAATAACAGTTAGTGG
AAATCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAAA
AAAAACGATTAATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACA
CGTTTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCA
ATTTCCCAATAAGTTTCATATTCAAGTTCAAGAAAAAAGATTATTGCA
TATGCACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAA
GCTGATCCTGTAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTA
CCTTGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCTT
TAGACCTGATTTAATAAGTGAAGATTGAGGTGATAAGTTTAGCTGATTCT
AAAACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTAT
TAGAATACCATTAATCTAAATTTAAGAAAGACTTCCTTTTACAAACAAA
TTAAGAAGAACCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGT
TACACAACAACAATAACCTTGAATCAACCCCTGTAAAGCAGAAGATAC
AAAAAATAAATCAACTGATAAAACACAACCCAAAATGGTCAGGTGCGG
AAAATAGTCAAGGACAAACAAATAACTCAAATACTAATCAACAGGACAA
CAGATAGCAACAGAGCAGGCACCTAACCTCAAATGTTAAT

SEQ ID NO. 8810

STRAIN A909

CCTAAGAAGAAATCAGATACCCCGAAAAAGAAGTGTGTC
TTAACGGAATGGCAAAAGCGTAACCTTGAATTTTaaAAAAACGCAAGA
AGATGAAGAAGaaCAAAAACGTATTACGAAAAATTACGCTTAGATAAAA
GAAGTAAATTAATATTTCTCTCCTGAAGAACCTCAAATACTACTATAA
ATTAAGAAAGCTTCATTTTCCAAAGATTTCAAGACCTAAGATTGAAAAGAA
ACAGAAAAAAGAAAAATAGTCAACAGCTTAGCCAAAATACTCGATTGA
GACTGACCTATATTGTAAGTAGCATTCTAGTCATTTAGTTTCCGTT
TTCCCTACTAATCCTTTTAGTAAGCAAAAACAATAACAGTTAGTGGAAA
TCAGCATACACCTGATGATATTTGATAGAGAAAAAGCAATATTCAAAAA
ACGATTAATTTCTTTCTTTAATTTTAAACATAAAGCTATTGAACAACCT
TTAGCTGCAGAAGATGTATGGGTAAAAACAGCTCAGATGACTTATCAATT
TCCCAATAAGTTTCATATTCAAGTTCAAGAAAAAAGATTATTGATATG
CACATACAAAGCAAGGATATCAACCTGTCTTGGAAACTGGAAAAAAGGCT
GATCCTGTAATAGTTCAGAGCTACCAAGCACTTCTTAACAATTAACCT
TGATAAGGAAGATAGTATTAAGCTATTAATTAAGATTAAAGGCTTTAG
ACCTGATTTAATAAGTGAAGATTGAGGTGATAAGTTTAGCTGATTCTAAA
ACGACACCTGACCTCCTGCTGTAGATATGCACGATGGAAATAGTATTAAs

Table 88: Comparative Sequences relating to SAG0477

AAATACCATTACTAAATTTAAAGAAAGACTTCCTTTTACAAAACAAATTA
AGAAGAACCCTTAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTAC
ACAACAACAAATACCATTGAATCAACCCTGTTAAAGCAGAGATACAAA
AAATAAATCAACTGATAAAACCAAAmCACAAAATGGTCAGGTTGCGGAAA
ATAGTCAAGGACAAACAATAACTCAAATACTAATCAACAAGGACCAACAG
ATAGCAACAGAGCAGCCCTAACCTCAAATGTTAAT

SEQ ID NO. 8811
STRAIN 090

TAAGAAGAAATCAGATACCCAGAAAAAGAAGTGTCTTAACGGAAAT
GGCAAAAGCGTAACCTTGAATTTTAAAAAACGCAAGAAGATGAAGAA
GAACAAAAACGTATTAAAGAAAAATACGCTTAGATAAAAGAAAGTaaATT
AAATATTCTTCTCCTGAAGAACCTCAAATACTACTAAAATTAAAGAAGC
TTCATTTTCCAAGATTTCAAAACCTAAGATTGAAAAGAAACGAAAAAAA
GAAAAAATAGTCAACAGCTTAGCCAAAACCTAATCGCATTAGAAGTGCACC
TATATTTGTAGTAGCATTCTAGTCAATTTAGTTTCCGTTTTCCTACTAA
CTCCTTTTAGTAAAGCAAAAACAAATAACAGTTAGTGGAAATCAGCATAACA
CCTGATGATATTTTATAGAAAAAACGAATATTCAAAAAACGATTATTT
CTTTCTTTAATTTTAAACATAAAGCTATTGAACAACGTTTAGCTGCAG
AAGATGTATGGGTA AAAACAGCTCAGATGACTTATCAATTTCCCAATAAG
TTTCATATTCAAGTTCAAGAAAATAAGATTATGATATGCACATACAAA
GCAGGATATCAGCCTGTCTTGGAAACGGA AAAAGGCTGATCCTGTAA
ATAGTTCAGAGCTACCAAGCACTTCTTAACAATTAACCTTGATAAGGAA
GATAGTATTAAGCTATTAATTAAGATTAAAGGCTTAGACCCTGATTT
AATAAGTGAGATTCAAGGTGATAAGTTTAGCTGATCTAAAACGACACTG
ACCTCCTGCTGTAGATATGATGATGAAATAGTATTAGAATACCAITTA
TCTAAATTTAAAGAAAGACTTCTCTTTTACAAAACAATTAAGAAGAACTT
TAAGGAACCTTCTATTGTTGATATGGAAGTGGGAGTTTACACAACAACA
GTACTATTGAATCAACCCTGTGAAAGCGGAAGATACAAAAATAAATCA
ACTGATAAAAACAACAACAATAAGTTCAGGTTGCGGAAAATAGTCAAGG
ACAAACAATAACTCAAATACTAATCAACAAGGACACAGATAGCAACAG
AGCAGGCACCAACCTCAAATGTTAAT

PRETTY of: /biotmp/msa24691.2{*} August 5, 2002 05:14 ..

1 50
msa252409.2{85_090.con } --TAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_CJB110 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_COH1 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_M732 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_M781 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_18RS21 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_2603 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_A909 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_H36B } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_JM9130013 } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
msa252409.2{85_1169NT } CCTAAGAAGA AATCAGATAC CCCAGAAAA GAAGAAGTTG TCTTAACGGA
Consensus *****

51 100
msa252409.2{85_090.con } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_CJB110 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_COH1 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_M732 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_M781 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_18RS21 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_2603 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_A909 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_H36B } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_JM9130013 } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
msa252409.2{85_1169NT } ATGGCAAAAG CGTAACCTTG AATTTTTAAA AAAACGCAAA GAAGATGAAG
Consensus *****

101 150
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msa252409.2{85_CJB110 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_COH1 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_M732 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_M781 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_18RS21 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_2603 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_A909 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_H36B } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_JM9130013 } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
msa252409.2{85_1169NT } AAGAACA AAA ACGTATTAAC GAAAAATTAC GCTTAGATAA AAGAAGTAAA
Consensus *****

151 200
msa252409.2{85_090.con } TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
msa252409.2{85_CJB110 } TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
msa252409.2{85_COH1 } TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA
msa252409.2{85_M732 } TTAAATATTT CTCTCCTGA AGAACCTCAA AATACTACTA AAATTAAGAA

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M781}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_18RS21}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_2603}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_A909}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_H36B}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_JM9130013}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
msa252409.2{85_1169NT}	TTAAATATTT	CTTCTCCTGA	AGAACCTCAA	AATACTACTA	AAATTAAGAA
Consensus	*****	*****	*****	*****	*****
201					
msa252409.2{85_090.con}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_CJB110}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_COH1}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M732}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_M781}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_18RS21}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_2603}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_A909}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_H36B}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_JM9130013}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
msa252409.2{85_1169NT}	GCTTCATTTT	CCAAAGATTT	CAAaACCTAA	GATTGAAAAG	AAACAGAAAA
Consensus	*****	*****	***-*****	*****	*****
251					
msa252409.2{85_090.con}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_CJB110}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_COH1}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_M732}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_M781}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_18RS21}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_2603}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_A909}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_H36B}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_JM9130013}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
msa252409.2{85_1169NT}	AAGAAAAAAT	AGTCAACAGC	TTAGCCAAAA	CTAATCGCAT	TAGAAGTGA
Consensus	*****	*****	*****	*****	*****
301					
msa252409.2{85_090.con}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_CJB110}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_COH1}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_M732}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_M781}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_18RS21}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_2603}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_A909}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_H36B}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_JM9130013}	CCTATATTTg	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
msa252409.2{85_1169NT}	CCTATATTTa	TAGTAGCATT	CCTAGTCATT	TTAGTTTCCG	TTTTCCCTACT
Consensus	*****	*****	*****	*****	*****
351					
msa252409.2{85_090.con}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_CJB110}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_COH1}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M732}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_M781}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_18RS21}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_2603}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_A909}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_H36B}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_JM9130013}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
msa252409.2{85_1169NT}	AACTCCTTTT	AGTAAGCAAA	AAACAATAAC	AGTTAGTGGA	AATCAGCATA
Consensus	*****	*****	*****	*****	*****
401					
msa252409.2{85_090.con}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_CJB110}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_COH1}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M732}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_M781}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_18RS21}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_2603}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_A909}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_H36B}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_JM9130013}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
msa252409.2{85_1169NT}	CACCTGATGA	TATTTTGATA	GaAAAAACGA	ATATTCAAAA	AAACGATTAT
Consensus	*****	*****	**-*****	*****	*****
451					
msa252409.2{85_090.con}	TTCTTTTCTT	TAATTTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_CJB110}	TTCTTTTCTT	TAATTTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_COH1}	TTCTTTTCTT	TAATTTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_M732}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_M781}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_18RS21}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_2603}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_A909}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_H36B}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_JM9130013}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
msa252409.2{85_1169NT}	TTCTTTTCTT	TAATTTTAA	ACATAAAGCT	ATTGAACAAC	GTTTAGCTGC
Consensus	*****	*****	*****	*****	*****
501					
msa252409.2{85_090.con}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_CJB110}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_COH1}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_M732}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_M781}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_18RS21}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_2603}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_A909}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_H36B}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_JM9130013}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
msa252409.2{85_1169NT}	AGAAGATGTA	TGGGTAATAA	CAGCTCAGAT	GACTTATCAA	TTTCCCAATa
Consensus	*****	*****	*****	*****	*****
551					
msa252409.2{85_090.con}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_CJB110}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_COH1}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_M732}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_M781}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_18RS21}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_2603}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_A909}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_H36B}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_JM9130013}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
msa252409.2{85_1169NT}	AGTTTCATAT	TCAAGTTCAA	GAAAATAAGA	TTATTGCATA	TGCACATACA
Consensus	*****	*****	*****	*****	*****
601					
msa252409.2{85_090.con}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_CJB110}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_COH1}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_M732}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_M781}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_18RS21}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_2603}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_A909}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_H36B}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_JM9130013}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
msa252409.2{85_1169NT}	AAGCAAGGAT	ATCAGCCTGT	CTTGAAACT	GGAAAAAAGG	CTGATCCTGT
Consensus	*****	*****	*****	*****	*****
651					
msa252409.2{85_090.con}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_CJB110}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_COH1}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_M732}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_M781}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_18RS21}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_2603}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_A909}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_H36B}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_JM9130013}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
msa252409.2{85_1169NT}	AAATAGTTCA	GAGCTACCAA	AGCACTTCTT	AACAATTAAC	CTTGATAAGG
Consensus	*****	*****	*****	*****	*****
701					
msa252409.2{85_090.con}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_CJB110}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_COH1}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_M732}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_M781}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_18RS21}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_2603}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_A909}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_H36B}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_JM9130013}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
msa252409.2{85_1169NT}	AAGATAGTAT	TAAGCTATTA	ATTAAAGATT	TAAAGGCTTT	AGACCCCTGAT
Consensus	*****	*****	*****	*****	*****
751					
msa252409.2{85_090.con}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_CJB110}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_COH1}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M732}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_M781}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_18RS21}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_2603}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_A909}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_H36B}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_JM9130013}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
msa252409.2{85_1169NT}	TTAATAAGTG	AGATTCAGGT	GATAAGTTTA	GCTGATTCTA	AAACGACACC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_CJB110}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_COH1}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_M732}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_M781}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_18RS21}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_2603}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_A909}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_H36B}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_JM9130013}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
msa252409.2{85_1169NT}	TGACCTCCTG	CTGTTAGATA	TGCAtGATGG	AAATAGTATT	AgAATACCAT
Consensus	*****	*****	***-****	*****	*-*****
msa252409.2{85_090.con}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_CJB110}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_COH1}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M732}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_M781}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_18RS21}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_2603}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_A909}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_H36B}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_JM9130013}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
msa252409.2{85_1169NT}	TATCTAAATT	TAAAGAAAGA	CTTCCTTTTT	ACAAACAAAT	TAAGAAGAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_CJB110}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_COH1}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_M732}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_M781}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_18RS21}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_2603}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_A909}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_H36B}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_JM9130013}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
msa252409.2{85_1169NT}	CITTAAGGAAC	CTTCTATTGT	TGATATGGAA	GTGGGAGTTT	ACACAACAAC
Consensus	*****	*****	*****	*****	*****
msa252409.2{85_090.con}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_CJB110}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_COH1}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M732}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_M781}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
msa252409.2{85_18RS21}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_2603}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_A909}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_H36B}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_JM9130013}	AAaTACcATT	GAATCAACCC	CTGTtAAAGC	aGAAGATACA	AAAAATAAAT
msa252409.2{85_1169NT}	AAgTACTATT	GAATCAACCC	CTGTgAAAGC	gGAAGATACA	AAAAATAAAT
Consensus	**--***-***	*****	***-****	-*****	*****
msa252409.2{85_090.con}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_CJB110}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_COH1}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M732}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_M781}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_18RS21}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_2603}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_A909}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_H36B}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_JM9130013}	CAACTGATAA	AACACAAaCa	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
msa252409.2{85_1169NT}	CAACTGATAA	AACACAAaCc	CAAAATGGTC	AGGTTGCGGA	AAATAGTCAA
Consensus	*****	*****-*	*****	*****	*****
msa252409.2{85_090.con}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC

Table 88: Comparative Sequences relating to SAG0477

msa252409.2{85_CJB110}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_COH1}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M732}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_M781}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_18RS21}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_2603}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_A909}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_H36B}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_JM9130013}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGG...AC	AACAGATAGC
msa252409.2{85_1169NT}	GGACAAACAA	ATAACTCAA	TACTAATCAA	CAAGGacaAC	AACAGATAGC
Consensus	*****	*****	*****	*****	*****

	1101		1134
msa252409.2{85_090.con}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_CJB110}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_COH1}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_M732}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_M781}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_18RS21}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_2603}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_A909}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_H36B}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_JM9130013}	AACaGAGCAG	GCACCcAACC	CTCAAAATGT
msa252409.2{85_1169NT}	AACgGAGCAG	GCACCcAACC	CTCAAAATGT
Consensus	***-*****	*****-****	*****

SEQ ID NO. 8812

STRAIN 2603 frame: 1

PKKKS DTP EKEE VVL TEWQKR NLEFLK KRKEDEEEQKR INEKLRLDKRSKLN I SSP EEPQ
 N TTKI KKLHFPKI SRPKIEKKQKKEKI VNSLAKTNR I RTAPI FVVAFLV I LVSVFLLT PF
 SKQRTITVSGNQHTPDD I LI EKTNI QKNDYFFSLI FKHKAEQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV I SLADSKTTPDLLLDMHDGNS I R I PLSKFKERLPFYKQ I KKN
 LKEPS IVDMEVG VYTTNT I ESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNN SNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8813

STRAIN H36B frame: 1

PKKKS DTP EKEE VVL TEWQKR NLEFLK KRKEDEEEQKR INEKLRLDKRSKLN I SSP EEPQ
 N TTKI KKLHFPKI SRPKIEKKQKKEKI VNSLAKTNR I RTAPI FVVAFLV I LVSVFLLT PF
 SKQRTITVSGNQHTPDD I LI EKTNI QKNDYFFSLI FKHKAEQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV I SLADSKTTPDLLLDMHDGNS I R I PLSKFKERLPFYKQ I KKN
 LKEPS IVDMEVG VYTTNT I ESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNN SNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8814

STRAIN 18RS21 frame: 1

PKKKS DTP EKEE VVL TEWQKR NLEFLK KRKEDEEEQKR INEKLRLDKRSKLN I SSP EEPQ
 N TTKI KKLHFPKI SRPKIEKKQKKEKI VNSLAKTNR I RTAPI FVVAFLV I LVSVFLLT PF
 SKQRTITVSGNQHTPDD I LI EKTNI QKNDYFFSLI FKHKAEQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV I SLADSKTTPDLLLDMHDGNS I R I PLSKFKERLPFYKQ I KKN
 LKEPS IVDMEVG VYTTNT I ESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNN SNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8815

STRAIN M732 frame: 1

PKKKS DTP EKEE VVL TEWQKR NLEFLK KRKEDEEEQKR INEKLRLDKRSKLN I SSP EEPQ
 N TTKI KKLHFPKI SRPKIEKKQKKEKI VNSLAKTNR I RTAPI FVVAFLV I LVSVFLLT PF
 SKQRTITVSGNQHTPDD I LI EKTNI QKNDYFFSLI FKHKAEQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV I SLADSKTTPDLLLDMHDGNS I R I PLSKFKERLPFYKQ I KKN
 LKEPS IVDMEVG VYTTNT I ESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNN SNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8816

STRAIN COH1 frame: 1

PKKKS DTP EKEE VVL TEWQKR NLEFLK KRKEDEEEQKR INEKLRLDKRSKLN I SSP EEPQ
 N TTKI KKLHFPKI SRPKIEKKQKKEKI VNSLAKTNR I RTAPI FVVAFLV I LVSVFLLT PF
 SKQRTITVSGNQHTPDD I LI EKTNI QKNDYFFSLI FKHKAEQR LAEDVWVKTAQMTYQ
 FPNKFHI QVQENKI IAYAHTKQGYQPVLETGKKADPVNSSEL PKHFLTINLDKEDSI KLL
 IKDLKALDPDLI SEIQV I SLADSKTTPDLLLDMHDGNS I R I PLSKFKERLPFYKQ I KKN
 LKEPS IVDMEVG VYTTNT I ESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGQTNN SNTNQ
 QGQQIATEQAPNPQNVN

SEQ ID NO. 8817

STRAIN M781 frame: 1

PKKKS DTP EKEE VVL TEWQKR NLEFLK KRKEDEEEQKR INEKLRLDKRSKLN I SSP EEPQ

Table 88: Comparative Sequences relating to SAG0477

NTTKIKLHFPFKISPKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTIIVSGNQHTPDDILLIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPLDISEIQVIVSLADSKTTPDLLLDMHDGNSIRIPLSKFKERLFPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGTNNSTNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8818

STRAIN CJB110 frame: 1

PKKKSDTPEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKLHFPFKISPKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTIIVSGNQHTPDDILLIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPLDISEIQVIVSLADSKTTPDLLLDMHDGNSIRIPLSKFKERLFPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGTNNSTNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8819

STRAIN 1169NT frame: 1

PKKKSDTPEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKLHFPFKISPKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTIIVSGNQHTPDDILLIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPLDISEIQVIVSLADSKTTPDLLLDMHDGNSIRIPLSKFKERLFPFYKQIKKN
LKEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGTNNSTNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8820

STRAIN JM9130013 frame: 1

PKKKSDTPEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKLHFPFKISPKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTIIVSGNQHTPDDILLIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPLDISEIQVIVSLADSKTTPDLLLDMHDGNSIRIPLSKFKERLFPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGTNNSTNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8821

STRAIN A909 frame: 1

PKKKSDTPEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
NTTKIKLHFPFKISPKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
SKQKTIIVSGNQHTPDDILLIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
FPNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLL
IKDLKALDPLDISEIQVIVSLADSKTTPDLLLDMHDGNSIXIPLSKFKERLFPFYKQIKKN
LKEPSIVDMEVGVYTTTNTIESTPVKAEDTKNKSTDKTQXNGQVAENSQGGTNNSTNTNQ
QGQQIATEQAPNPQNVN

SEQ ID NO. 8822

STRAIN 090 frame: 2

KKKSDTPEKEEVLTEWQKRNLEFLKRRKEDEEEQKRINEKLRLDKRSKLNISSPEEPQ
TTTKIKLHFPFKISPKPKIEKKQKKEKIVNSLAKTNRIRTAPIFVVAFLVILVSVFLLTPF
KQKTIIVSGNQHTPDDILLIEKTNIQKNDYFFSLIFKHKAIEQRLAAEDVWVKTAQMTYQ
PNKFHIVQVENKI IAYAHTKQGYQPVLETGKKADPVNSSELPKHFLTINLDKEDSIKLLI
KDLKALDPLDISEIQVIVSLADSKTTPDLLLDMHDGNSIRIPLSKFKERLFPFYKQIKKNL
KEPSIVDMEVGVYTTTSTIESTPVKAEDTKNKSTDKTQTQNGQVAENSQGGTNNSTNTNQ
QGQQIATEQAPNPQNVN

PRETTY of: /biotmp/msa252337.2{*} January 31, 2003 03:32 ..

Table with 2 columns (51 and 100) and multiple rows of sequence alignments for various strains including msa252337.2{85_090}, msa252337.2{85_18RS21}, msa252337.2{85_2603}, msa252337.2{85_A909}, msa252337.2{85_CJB110}, msa252337.2{85_COH1}, msa252337.2{85_H36B}, msa252337.2{85_JM9130013}, msa252337.2{85_M732}, msa252337.2{85_M781}, msa252337.2{85_1169NT}, and Consensus. The table shows sequence alignments for two different positions (51 and 100) across these various strains.

Table 88: Comparative Sequences relating to SAG0477

msa252337.2{85_COH1}	LNISSPPEEPQ	NTTKIKKLLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_H36B}	LNISSPPEEPQ	NTTKIKKLLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_JM9130013}	LNISSPPEEPQ	NTTKIKKLLHF	PKISrPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M732}	LNISSPPEEPQ	NTTKIKKLLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_M781}	LNISSPPEEPQ	NTTKIKKLLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
msa252337.2{85_1169NT}	LNISSPPEEPQ	NTTKIKKLLHF	PKISkPKIEK	KQKKEKIVNS	LAKTNRIRTA
Consensus	*****	*****	****_****	*****	*****
101					
msa252337.2{85_090}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_18RS21}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_2603}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_A909}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_CJB110}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_COH1}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_H36B}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_JM9130013}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M732}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_M781}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
msa252337.2{85_1169NT}	PIFvVAFVLI	LVSFVLLTPF	SKQKTITVSG	NQHTPDDILI	EKTNIQKNDY
Consensus	***_****	*****	*****	*****	*****
151					
msa252337.2{85_090}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_2603}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_A909}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_CJB110}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_COH1}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_H36B}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M732}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M781}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_1169NT}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
Consensus	*****	*****	*****	*****	*****
200					
msa252337.2{85_090}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_18RS21}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_2603}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_A909}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_CJB110}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_COH1}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_H36B}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_JM9130013}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M732}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_M781}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
msa252337.2{85_1169NT}	FFSLIFKHKA	IEORLAAEDV	VWIKTAQMTYQ	FPNKFHIQVQ	ENKI IAYAHT
Consensus	*****	*****	*****	*****	*****
201					
msa252337.2{85_090}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_18RS21}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_2603}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_A909}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_CJB110}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_COH1}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_H36B}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_JM9130013}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M732}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_M781}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
msa252337.2{85_1169NT}	KQGYQPVLET	GKKADPVNSS	ELPKHFLTIN	LDKEDSIKLL	IKDLKALDPD
Consensus	*****	*****	*****	*****	*****
251					
msa252337.2{85_090}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_18RS21}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_2603}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_A909}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	xIPLSKFKER	LFFYKQIKKN
msa252337.2{85_CJB110}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_COH1}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_H36B}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_JM9130013}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_M732}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_M781}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
msa252337.2{85_1169NT}	LISEIQVISL	ADSKTTPDLL	LLDMHDGNSI	rIPLSKFKER	LFFYKQIKKN
Consensus	*****	*****	*****	-*****	*****
301					
msa252337.2{85_090}	LKEPSIVDME	VGYYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_18RS21}	LKEPSIVDME	VGYYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_2603}	LKEPSIVDME	VGYYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_A909}	LKEPSIVDME	VGYYTTTnTI	ESTPVKAEDT	KNKSTDKTQx	QNGQVAENSQ
msa252337.2{85_CJB110}	LKEPSIVDME	VGYYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_COH1}	LKEPSIVDME	VGYYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_H36B}	LKEPSIVDME	VGYYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_JM9130013}	LKEPSIVDME	VGYYTTTnTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M732}	LKEPSIVDME	VGYYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_M781}	LKEPSIVDME	VGYYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
msa252337.2{85_1169NT}	LKEPSIVDME	VGYYTTTtTI	ESTPVKAEDT	KNKSTDKTQc	QNGQVAENSQ
Consensus	*****	*****_**	*****	*****_	*****
351					
msa252337.2{85_090}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-	378	
msa252337.2{85_18RS21}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-		
msa252337.2{85_2603}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-		
msa252337.2{85_A909}	GQTNNSENTNQ	QGQQiateqa	pnpqnv-		

Table 88: Comparative Sequences relating to SAG0477

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msa252337.2{85_CJB110} GQTNNSNTNQ QGQQiateqa pnpqrvn-
msa252337.2{85_COH1} GQTNNSNTNQ QGQQiateqa pnpqrvn-
msa252337.2{85_H36B} GQTNNSNTNQ QGQQiateqa pnpqrvn-
msa252337.2{85_JM9130013} GQTNNSNTNQ QGQQiateqa pnpqrvn-
msa252337.2{85_M732} GQTNNSNTNQ QGQQiateqa pnpqrvn-
msa252337.2{85_M781} GQTNNSNTNQ QGQQiateqa pnpqrvn-
msa252337.2{85_1169NT} GQTNNSNTNQ QGQQiateq apnpqrvn
Consensus ***** *****-----*

```

Table 89: Comparative Sequences relating to SAG1350

SEQ ID NO. 8901
 STRAIN 2603
 ATGAAAAAAGGACAAGTAAATGATACTAAGCAATCTTACTCTCTACGTAAA
 TATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTCATAATGGTCACAAGCTCTGT
 TTTGCGGATCAAACCTACATCGGTTCAAGTTAATAATCAGACAGGCCTAGTGTGGATGCT
 AATAATCTTCCAATGAGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGT
 CAAGCGTCTGATAAAGTTGTAANTAGTCAAATACGGCAACAAAGGACATTACTACTCCT
 TTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAACAAGGGAATTTATGTTTAT
 AGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCA
 AAGAAAGGTGATAAAGTTTCTATGACCAAGTATTTAATAAAGATAATGTGAAATGGATT
 TCATATAAGTCTTTTGTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCA
 GGAGGTTTCAGAGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
 AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAAAAATGAAGCT
 AAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAGGAGACAGAATTTTTTACGCCAA
 ATACTAATCTATTGAAGGAAATCAGTGGTTATCTTTATAAATCAITCAATGGTGTTCGCT
 TTTGTTTTGTAGTAAAGCATCTTCACTAGAAAAAATGAAGATAAAGAAAAAGTGTCT
 CCTCAACCAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACT
 ACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCGCTGCTGTTAAG
 GTACCGGTTTGGACTGAAACAAGGAGGCAAGATGATATTAAATGGTATACAGCTGTAAT
 ACTGGGGATGGCAACTCAAAAGTAGCTGTATCATTTGCTGACCATAAAGATGAGAAGGGT
 CTTTATAATATTCATTTATACTACCAAGAGCTAGTGGGACACTTTGTAGGTGTAAACAGGA
 ACTAAAGTGACAGTAGCTGGAACTAATTTCTCTCAAGAACCTATTGAAAAAGGTTTAGCA
 AAGACTGGTGTTTAATAATTTATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCA
 AGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAATAAATATGATCAAGTATTGACA
 GCAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTCGCTATATTCCT
 GTGAAAAAGCTAACTACAGTAGTGAAGAAAGCGAAAGATGAGGCGACTAAACCGACTAGT
 TATCCCAACTTACCTAAAAACAGGTACCTATACATTTACTAAAACTGTAGATGTGAAAAGT
 CAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTAAAAAATACATTAT
 GATCAAGTGTTAGTAGTAGATGGTCACTCAGTGGATTTTCATACAAGAGTTATTCGGTATT
 CGTCGCTATATTGAAATT

SEQ ID NO. 8902
 STRAIN 090
 AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
 CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 ATAATGGTCAACAGTCCCTGTTTTTGGCGATCAAACCTACATCGGTTCAAGT
 TAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAGA
 CAAGTCCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 GATAAAGTTGTAATAGTCAAATACGGCAACAAAGGACATTACTACTCC
 TTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAAACAAGGGA
 ATTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
 GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCA
 AGTATTTAATAAAGATAATGTGAAATGGATTTCAATAAAGTCTTTTTGTG
 GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
 GAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGA
 GAAAAATAGCAACGCAAGGAAATATAACATTTTCACATAAAGTAGAAGTAA
 AAAATGAAGCTAAGTAGCGAGTCCAACCTCAATTTACATTTGGACAAAGGA
 GACAGAATTTTTTACGACCAAATACTAATTTGAAGGAAATCAGTGGTT
 ATCTTATAAATCAITCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAG
 CATCTTCAGTAGAAAAAATGAAGATAAAGAAAAAGTGTCTCCTCAACCA
 CAAGCCCGTATTACTAAAACTGGTAGACTGACTATTTCTAACGAAACAACT
 TACAGGTTTTGATATTTAATTACGAATATTAAAGATGATAACGGTATCG
 CTGCTGTTAAGGTACCGGTTTGGACTGAAACAAGGAGGCAAGATGATATT
 AAATGGTATACAGCTGTAACCTATGGGGATGGCAACTACAAGTAGCTGT
 ATCATTTGCTGACCATAAAGATGAGAAGGGTCTTTATAATATTCAATTTAT
 ACTAACGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTG
 ACAGTAGCTGGAACATAATCTTCTCAAGACCTATTGAAAATGGTTTAGC
 AAAGACTGGTGTTTATAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
 CTAAAAATCAAGTCAAGTCAAGCCAAATTTACTTTAGAAAAAGGTGACAAAAATA
 AATTTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
 ATCTTATAGTGGTGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAA
 GTAGTAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
 TTACCTAAAAACAGGTACTTATACATTTACTAAAACTGTAGATGTGAAGAG
 TCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTCAAAGGGTGA
 AAATACTATTGATCAAGTGTAGTAGTAGATGGTCACTCAGTGGATTTCA
 TACAAGAGTTATTCGGTATTTCGTCGCTATATTGAAATT

SEQ ID NO. 8903
 STRAIN A909
 AAAAAAGGACAAGTAAATGATACTAAGCAATCTTAC
 TCTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATT
 CATTAATGGTCAACAGTCCCTGTTTTTGGCGATCAAACCTACATCGGTTCAAG
 TTAATAATCAGACAGGCCTAGTGTGGATGCTAATAATCTTCCAATGAG
 ACAAGTCCGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
 TGATAAAGTTGTAATAAGTCAAATACGGCAACAAAGGACATTACTACTC
 CTTTAGTAGAGACAAAGCCAAATGGTGGAAAAACATTACCTGAAACAAGG
 AATTTAGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATC
 AGCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACC
 AAGTATTTAATAAAGATAATGTGAAATGGATTTCAATAAAGTCTTTTTGT
 GCGTACGTCGATACGCAGCTATTGAGTCACTPAGATCCATCAGGAGGTT
 AGAGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAG
 AGAAAAATGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTA
 AAAAAAGGCTAAGGTAGCGAGTCCAACCTCAATTTACATTTGACAAAGG

Table 89: Comparative Sequences relating to SAG1350

AGACAGAATTTTTACGACCAAATACTAATATTGAAGGAAATCAGTGGT
TATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAA
GCATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACC
ACAAGCCCGTATTACTAAAACCTGGTAGACTGACTAATTTCTAACGAAACAA
CTACAGGTTTTGATATTTAATTAACGAATATTAAGATGATAACCGGTATC
GCTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATAT
TAAATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAGTAGCTG
TATCATTGCTGACCATAAAGATGAGAAGGGTCTTTATAATATTCATTTA
TACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAAACAGGAACTAAAGT
GACAGTAGCTGGAACTAATCTTCTCAAGAACCCTATTGAAAATGGTTTAG
CAAAGACTGGTGTTTATAATAATTATCGGAAGTACTGAAGTAAAAAATGAA
GCTAAAATATCAAGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAAT
AAAATATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACA
AATCTTATAGTGGTGTTCGTGCTATATTTCTGTGAAAAAGCTAACTACA
AGTAGTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAA
CTTACCTAAAACAGGTACTTATACATTTACTAAAACCTGTAGATGTGAAGA
GTC AACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGAA
AAAAATACATTTATGATCAAGTGTTAGTAGATGGTCTACAGTGGATTTT
ATACAAGAGTTATTCCGGTATTCTGTCGCTATATTGAAATTT

SEQ ID NO. 8904

STRAIN H36B

AAAAAAGGCAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTTC
ATAATGGTCAACAAGTCTGTTTTTGGCGGATCAAACACTACATCGGTTCAAGT
TAATAATCAGACAGGCACTAGTGTGGATGATAAATTTCTTCCAATGAGA
CAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCT
GATAAAGTTGTAATAGTCAAATACGGCAACAAAGGCACTTACTACTCC
TTTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGA
ATTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAAATGTGAAATGGATTTCAATAAAGTCTTTTTGTG
GCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCAAGA
GAAAAATAGCAACCGCAAGGAAATATAACATTTTCAATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTTGGACAAAGGA
GACAGAATTTTTACGACCAAATACTAATTTGAAGGAAATCAGTGGTT
ATCTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAG
CATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCGTTATTACTAAAACCTGGTAGACTGACTAATTTCAACGAAACAAC
TACAGGTTTTGATATTTAATTACGAATATTAAGATGATAACGGTATCG
CTGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACACTCTGGGATGGCAACTACAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAAATTTCAATTTAT
ACTACCAAGAAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGT
ACAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAATGGTTTTAGC
AAAGACTGGTTTTATAAATTTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA
AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTGCTATATTTCTGTGAAAAAGCTAACTACAA
GTAGTAAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACTTATAATTTACTAAAACCTGTAGATGTGAAGAG
TCAACCTAAAAGTATCAAGTCCAGTGGAAATTAATTTCAAAGGGTGAAA
AAATACATTTATGATCAAGTGTTAGTAGTAGATGGTCTACAGTGGATTTCA
TACAAGAGTTATTCCGGTATTCTGTCGCTATATTGAAATTT

SEQ ID NO. 8905

STRAIN 18RS21

AAAAAAGGCAAGTAAATGATACTAAGCAATCTTACTC
TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTCA
TAATGGTCAACAAGTCTGTTTTTGGCGGATCAAACACTACATCGGTTCAAGTT
AATAATCAGACAGGCACTAGTGTGGATGCTAATAATTTCTTCCAATGAGAC
AAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTG
ATAAAGTTGTAATAAGTCAAATAACCGCAACAAAGGACATTACTACTCCT
TTAGTAGAGCAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGAA
TTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCAG
CCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCAA
GTATTTAATAAAGATAATGTGAAATGGATTTCAATAAAGTCTTTTTGTGG
CGTAGCTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTGAG
AGACTAAAGCACCTACTCCTGTAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACCGCAAGGAAATATAACATTTTCAATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTAATTGGACAAAGGAG
ACAGAATTTTTACGACCAAATACTAATTTGAAGGAAATCAGTGGTTA
CTTTATAAATCATTCAATGGTGTTCGTGTTTTGTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAAGTGAAGATAAAGAAAGTGTCTCCTCAACCAC
AAGCCCGTATTACTAAAACCTGGTAGACTGACTAATTTCAACGAAACAAC
ACAGGTTTTGATATTTAATTAACGAATATTAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACACTCTGGGATGGCAACTACAAGTAGCTGTA
TCATTTGCTGACCATAAAGATGAGAAGGGTCTTTATAAATTTCAATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAAACAGGAACTAAAGTGA
CAGTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAAGTTTAGCA
AAGACTGGTGTTTATAAATTTATCGGAAGTACTGAAGTAAAAAATGAAGC

Table 89: Comparative Sequences relating to SAG1350

TAAAAATCAAGTCAGACCCCAATTTACTTTAGAAAAAGGTGACAAAATAA
ATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAAA
TCCTTAGTGGTTCGTCGCTATATTCCTGTGAAAAAGCTAACTACAAG
TAGTAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACT
TACCTAAAACAGGTACCTATACATTTACTAAAACGTAGATGAAAAAGT
CAACCTAAAGTATCAAGTCCAGTGGAAATTTAAATTTCAAAGGGTGAAAA
AATACHTTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTTCAT
ACAAGAGTTATTCGGTATTCGTGCTATATTGAAATT

SEQ ID NO. 8906

STRAIN M732

CAAGTAAATGATaCTAAGCAATCTTACTCTCTACGTAATATAAATTGG
TTTAGCATCAGTAATTTAGGGTCATTATAATGGTCACAAGTCCTGTTT
TTGCCGATCAAACTACATCGGTTCAAGTTAATAATCAGACAGGCACTAGT
GTGGATGCTAATAAATCTTCCAATGAGACAAGTCCGTCAAGTGTGATTAC
TTCCAATAATGATAGTGTCAAGCGTCTGATAAAGTTGTAATAAGTCAAA
ATACCGCAACAAAGGACATTACTACTCCTTTAGTAGAGCAAAGCCAATG
GTGAAAAAACAATACCTGAACAAGGGAATATGTTTATAGCAAAGAAAC
CGAGGTGAAAAATACACCTTCAAATCAGCCCCAGTAGCTTTCTATGCAA
AGAAAGGTGATAAAGTTTTCTATGACCAAGTATTATAAAGATAATGTG
AAATGGATTTATATAAGTCTTTGGTGGCGTACGTCGATACGCAGCTAT
TGAGTCACTAGATCCATCAGGAGGTTCAAGAGACTAAAGCACCTACTCTG
TAACAAATTCAGGAAGCAATAATCAAGAGAAAAATAGCAACGCAAGGAAAT
TATACATTTTACATAAAGTAGAAGTAAAAATGAAGCTAAGGTAGCGAG
TCCAACCTCAATTTACATTTGGACAAAGGAGACAGAATTTTACGACCAA
TACTAATatTGAAGGAAATCAGTGGTTATCTTATAAATCATTCATGGT
GTTCTGCTTTTGTtTtLgCTAGGTAAGCATCTTCAGTAGAAAAAACTGA
AGATAAAGAAAAAGTGTCTCTCAACCACAAGCCGTTACTAAAACCTG
GTAGACTGACTATTTCTAACGAAACAACTACAGTCTTTGATATTTAATT
ACGAATATTAAGATGATAACGGTATCGCTGCTGTTAAGGTACCGGTTTG
GACTGAACAGGAGGGCAAGATGATATTAATGGTATACAGCTGTAACCTA
CTGGGGATGGCAACTCAAAAGTAGCTGTATCATTTGCTGACCATAGAAT
GAGAAGGCTCTTTATAAATTTATTATACTACCAAGAAGCTAGTGGGAC
ACTTGTAGGTGTAACAGGAACTAAAGTGAAGTAGCTGGAACATAATCTT
CTCAAGAACCTATTTGAAAATGGTTTACCAAAGACTGGTGTTTATAAATTT
ATCGGAAGTACTGAAGTAAAAAATGAAGCTAAAAATATCAAGTCAAGCCCA
ATTTACTTTAGAAAAAGGTGACAAAATAAATATGATCAAGTATTGACAG
CAGATGGTTACCAGTGGATTTCTTACAAATCTTATAGTGGTGTTCGTGCG
TATATTTCTGTGAAAAAGCTAACTACAAGTAGTAAAAAGCGAAAGATGA
GGCGACTAAACCGACTAGTTATCCCAACTTACCTAAACAGGTACCTATA
CATTTACTAAAACCTGATAGTGTGAAAAGTCAACCTAAAGTATCAAGTCCA
GTGGAATTTAATTTCAAAGGGTGAAAAATACATTTATGATCAAGTGTG
AGTAGTAGATGGTCATCAGTGGATTTCATACAAGAGTTATTCCGGTATTC
GTCGCTATATTGAAATT

SEQ ID NO. 8907

STRAIN COH1

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTCT
ACGTAATATAAATTTGGTTTAGCATCAGTAATTTAGGGTCATTATAA
TGGTCACAAGTCCGTGTTTGGCGGATCAAACTACATCGGTTCAAGTTAAT
AATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATGAGACAAG
TGCGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCTGATA
AAGTTGTAATAGTCAAATACGGCAACAAAGGACATTACTACTCTTTA
GTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAGGGAATTA
TGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCAGCCC
CAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCAAGTA
TTAATAAAGATAATGTTAAATGGATTTCAATATAAGTCTTTGGTGGCGT
ACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCAAGAGA
CTAAGCACCTATCTCTGTAACAAATTCAGGAAGCAATAATCAAGAGAAA
ATAGCAACGCAAGGAAATTTATACATTTTCAATATAAAGTAGAAGTAAAA
TGAAGCTAAGGTAGCGAGTCCAACCTCAATTTAATTGGAACAAGGAGACA
GAATTTTTACGACCAATACTAATATTGAAGGAAATCAGTGGTTATCT
TATAAATCATTCATGGTGTTCGTGCTTTGTTTGTCTAGGTAAAGCATC
TTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCACAAG
CCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACAACTACA
GGTTTTGATATTTAATTAAGAATATTAAGATGATAACGGTATCGCTGC
TGTTAAGGTACCGGTTTGGACTGAACAAGGAGGCAAGATGATTTAAAT
GGTATACAGCTGTAACTACTGGGGATGGCAACTACAAGTAGCTGTATCA
TTTGTGACCCATAAGAATGAGAAGGGTCTTTATAAATTTCAATTTATACTA
CCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAGTACAG
TAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAAATGGTTTACCAAAG
ACTGGTGTTTATAAATATATCGGAAGTACTGAAGTAAAAAATGAAGCTAA
AATATCAAGTCAAGCCCAATTTACTTTAGAAAAAGGTGACAAAATAAAT
ATGATCAAGTATTGACAGCAGATGGTTACCAAGTGGATTTCTTACAAATCT
TATAGTGGTGTTCGTGCTATATTTCTGTGAAAAAGCTAACTACAAGTAG
TGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTAC
CTAAAACAGGTACCTATACATTTACTAAAACCTGATAGTGTGAAAAAGTCAA
CCTAAAGTATCAAGTCCAGTGGAAATTTAATTTCAAAGGGTGAAAAAAT
ACATTTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCATACA
AGAGTTATTCCGGTATTCGTGCTATATTGAAATT

SEQ ID NO. 8908

STRAIN M781

Table 89: Comparative Sequences relating to SAG1350

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTT
 ACTCTCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCA
 TTCATAATGGTCAACAAGTCTGTGTTTGGCGATCAAACACATCGGTTCA
 AGTTAATAATCAGACAGGCACTAGTGTGGATGCTAATAATCTTCCAATG
 AGACAAGTGGTCAAGTGTGATTACTTCCAATAATGATAGTGTCAAGCG
 TCTGATAAAGTTGTAATAGTCAAATACGGCAACAAAGGACATTACTAC
 TCCTTTAGTAGAGACAAAGCCAATGGTGGAAAAACATTACCTGAACAG
 GGAATATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAAA
 TCAGCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGA
 CCAAGTATTTAATAAAGATAATGTGAATGGATTTCATATAAGTCTTTTG
 GTGGCGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGT
 TCAGAGACTAAAGCACCTACTCTGTAAACAAATTCAGGAAGCAATAATCA
 AGAGAAAATAGCAACGCAAGGAAATATACATTTTCCATAAAGTAGAAG
 TAAAAAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAA
 GGAGACAGAAATTTTACGACCAAATACTAATACTATGAAGGAAATCAGTG
 GTTATCTTATAAATCATTCATGGTGTTCGTCGTTTGTGTTTGTCTAGGTA
 AAGCATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAA
 CCACAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAAC
 AACTACAGGTTTGTATATTTAATTACGAATATTAAGATGATAACGGTA
 TCGCTGCTGTTAAGGTACCGGTTGGACTGAAACAGGAGGGCAAGATGAT
 ATTAATGGTATACAGCTGTAACACTCGGGGATGGCACTACAAAGTAGC
 TGTATCATTTGCTGACCCATAAGAATGAGAAGGGTCTTTATAATATTCATT
 TATACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAA
 GTGACAGTAGCTGGAACATAATTCTTCAAGAACCATTGAAAATGGTTTT
 ACCAAAGACTGGTGTTTATAATATTTACGGAAGTACTGAAGTAAAAATG
 AAGCTAAAATATCAAGTCAAGCCAAATTTACTTTAGAAAAAGGTGACAAA
 ATAAATATGATCAAGTATGACAGCAGATGGTTACCAGTGGATTTCTTA
 CAAATCTTATAGTGGTGTTCGTCGCTATATCTCTGTGAAAAAGCTAACTA
 CRAAGTAGTGA AAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCC
 AACTTACCTAAAACAGGTACCTATACATTTACTAAAACCTGATAGTGTGAA
 AAGTCAACCTAAAGTATCAAGTCCAGTGGAAATTTAATTTTCAAAGGGTG
 AAAAAATACATTTATGATCAAGTGTTAGTAGTAGATGGTCACTCAGTGGATT
 TCATACAAGAGTTATTCGGTATTCGTCGCTATATGAAATT

SEQ ID NO. 8909

STRAIN CJB110

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTCTC
 TACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCAATTCATA
 ATGGTCAACAAGTCTGTGTTTGGCGGATCAAACACATCGGTTCAAGTTAA
 TAATCAGACAGGCACTAGTGTGGATGCTAATAAATCTTCCAATGAGACAA
 GTGCGTCAAGTGTGATTACTTCCAATATGATAGTGTTCAGCGTCTGAT
 AAAGTTGTAATAGTCAAATACGGCAACAAAGGACATTACTACTCTTT
 AGTAGAGACAAAGCCAAATGGTGGAAAAAACATTACCTGAACAAAGGGAAT
 ATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATACAGCC
 CCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCAAGT
 ATTTAATAAAGATAATGTGAAATGGATTTCAATATAAGTCTTTTTGTGGCG
 TACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTCCAGAG
 ACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAGAA
 AATAGCAACGCAAGGAAATATACATTTTCAATAAAGTAGAAGTAAAAA
 ATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAGAC
 AGAATTTTTACGACCAAAATACTAACTATTGAAGGAAATCAGTGGTTATC
 TTATAAATCATTCATAGTGTTCGTCGTTTGTGTTTGTCTAGGTAAAGCAT
 CTTCAAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCACAA
 GCCCGTATTACTAAAACCTGGTAGACTGACTATTTCTAACGAAACCACTAC
 AGGTTTGTATTTTAAATACGAATATTAAGATGATAACGGTATCGCTG
 CTGTTAAGGTACCAGTTTGGACTGAAACAAGGAGGCAAGATGATATTA
 TGGTATACAGCTGTAACCTACTGGGGATGGCAACTACAAAGTAGCTGTATC
 ATTTGCTGACCATAGAATGAGAAGGGTCTTTATAATATTCATTTATACT
 ACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTGACA
 GTAGCTGGAACATAATCTTCTCAAGAACCTATTGAAAATGGTTTAGCAAA
 GACTGGTGTTTATAATATTTATCGGAAGTACTGAAGTAAAAAATGAAGCTA
 AAATATCAAGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAATAAAT
 TATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTCTTACAAATC
 TTATAGTGGTGTTCGTCGCTATATTTCTGTGAAAAAGCTAACTACAAAGTA
 GTGAAAAAGCGAAAGATGAGGCGACTAAACCGACTAGTTATCCCAACTTA
 CCTAAAACAGGTACCTATACATTTACTAAAACCTGATAGTGTGAAGAGTCA
 ACCTAAAGTATCAAGTCCAGTGGAAATTAATTTTCAAAGGGTGA AAAA
 TACATTTATGATCAAGTGTTAGTAGTAGATGGTCACTCAGTGGATTTTCATAC
 AAGAGTTATTCGGTATTCGTCGCTATATGAAATT

SEQ ID NO. 8910

STRAIN 1169NT

AAAAAAGGACAAAGTAAATGATACTAAGCAATCTTACTC
 TCTACGTAAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCAATTC
 TAATGGTCAACAAGTCTGTGTTTGGCGGATCAAACACATCGGTTCAAGTT
 AATAATCAGACAGGCACTAGTGTGGATGCTAATAAATCTTCCAATGAGAC
 AAGTCGTCAGAGTGTGATTACTTCCAATAATGATAGTGTTCAGCGTCTG
 ATAAAGTTGTAATAGTCAAATACGGCAACAAAGGACATTACTACTCTCT
 TTAGTAGAGACAAAGCCAATGGTGGAAAAAACATTACCTGAACAAAGGAA
 TTATGTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCAG
 CCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTCTATGACCAA
 GTATTTAATAAAGATAATGTGAAATGGATTTCATATAAGTCTTTTGGTGG
 CGTACGTCGATACGCAGCTATTGAGTCACTAGATCCATCAGGAGGTTACAG

Table 89: Comparative Sequences relating to SAG1350

AGACTAAAGCACCTACTCCTGTAAACAAATTCAGGAAGCAATAATCAAGAG
AAAATAGCAACGCAAGGAAATTTATACATTTTCACATAAAGTAGAAGTAAA
AAATGAAGCTAAGGTAGCGAGTCCAACCTCAATTTACATTGGACAAAGGAG
ACAGAATTTTACGACCAAACTACTACTATTGAAGGAAATCAGTGGTTA
TCTTATAAATCAATCAATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAAGC
ATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCTCAACCAC
AAGCCCGTATTACTAAACTGGTAGACTGACTATTTCTAACGAAACCACT
ACAGGTTTTGATATTTAATTAACGAATATTAAGATGATAACGGTATCGC
TGCTGTTAAGGTACCGGTTTTGGACTGAACAAGGAGGGCAAGATGATATTA
AATGGTATACAGCTGTAACACTGGGGATGGCAACTACAAAGTAGCTGTA
TCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAAATTCATTTATA
CTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACTAAAGTGA
CAGTAGCTGGAaCTAATTCCTCAAGAACCTATTGAAAAATGGTTTTAGCA
AAGACTGGTGTTTATAATAATTCGGAAGTACTGAAGTAAAAAATGAAGC
TAAAATATCAAGTCAGACCCAAATTTACTTTAGAAAAGGTGACAAAATAA
ATTATGATCAAGTATTGACAGCAGATGGTACCAGTGGATTTCTTACAAA
TCTTATAGTGGTGTTCGTCGTATATTCTGTGAAAAGCTAATACAAAG
TAGTGA AAAAGCGAAGATGAGGGCAGTAAACCGACTAGTTATCCCACT
TACCTAAAACAGGTACCTATACATTTACTAAAACCTGATAGTGA AAAAGT
CAACCTAAAGTATCAAGTCCAGTGGAAATTAATTTCAAAGGGTGAAAA
AATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCA
ACAAGAGTTATTCGGTATTCGTCGTATATTGAAAT

SEQ ID NO. 8911

STRAIN JM9130013

AAAAAAGGACAAGTAAATGATACTAAGCAATCTTACT
CTCTACGTAATATAAATTTGGTTTAGCATCAGTAATTTTAGGGTCATTC
ATAATGGTCACAAGTCTCTGTTTTGCGGATCAAACACTACATCGGTTCAAGT
TAATAATCAGACAGGCACCTAGTGTGGATGCTAATAATCTTCCAATGAGA
CAAGTCCGTCAGTGTGATTACTTCCAATAATGATAGTGTCAAGCGTCT
GATAAAGTTGTAATAGTCAAATAACGGCAACAAAGGACATTACTACTCC
TTTAGTAGAGACAAAGCCAAATGGTGGAAAAAACAATACCTGAAACAAGGGA
ATTATGTTTTATAGCAAAGAAACCGAGGTGAAAAATACACCTTCAAATCA
GCCCCAGTAGCTTTCTATGCAAAGAAAGGTGATAAAGTTTTCTATGACCA
AGTATTTAATAAAGATAATGTGAAATGGATTTCAATAAGTCTTTTTGTG
CGCTACGTCGATACCGACTTATGAGTCACTAGATCCATCAGGAGGTTCA
GAGACTAAAGCACCTACTCTCTGTAACAAATTCAGGAAGCAATAATCAAGA
GAAAATAGCAACGCAAGGAAATTTATACATTTTTCACATAAAGTAGAAGTAA
AAAATGAAGCTAAGGTAGCGAGTCCAACTCAATTTACATTTGGACAAAGGA
GACAGAATTTTTCGACCAAAATACTAATCTTGAAGGAATCAGTGGTT
ATCTTATAAATCATTCATGGTGTTCGTCGTTTTGTTTTGCTAGGTAAG
CATCTTCAGTAGAAAAAACTGAAGATAAAGAAAAAGTGTCTCCTCAACCA
CAAGCCCGTATTACTAAAACCTGGTAGACTGACTATTTATAACGAAACAAC
TACAGGTTTTGATATTTAATTAACGAATAATAAGATGATAACGGTATCCG
CTGCTTTAAGGTACCGGTTTGGACTGAACAAGGAGGGCAAGATGATATT
AAATGGTATACAGCTGTAACCTACTGGGGATGGCAACTCAAAGTAGCTGT
ATCATTTGCTGACCATAAGAATGAGAAGGGTCTTTATAAATTCATTTAT
ACTACCAAGAAGCTAGTGGGACACTTGTAGGTGTAACAGGAACATAAAGTG
ACAGTAGCTGGAACTAATTCCTCTCAAGAACCTATTGAAAATGGTTTAGC
AAAGACTGGTGTTTATAAATATTATCGGAAGTACTGAAGTAAAAAATGAAG
CTAAAATATCAAGTCAGACCCAAATTTACTTTAGAAAAAGGTGACAAAATA
AATTATGATCAAGTATTGACAGCAGATGGTTACCAGTGGATTTCTTACAA
ATCTTATAGTGGTGTTCGTCGTATATTCTCTGTGAAAAGCTAAGTACAA
GTAGTGA AAAAGCGAAGATGAGGGCAGTAAACCGACTAGTTATCCCAAC
TTACCTAAAACAGGTACCTATACATTTACTAAAACCTGTAGATGTGAAGAG
TCAACCTAAAGTATCAAGTCCAGTGGAAATTAATTTCAAAGGGTGAAA
AAATACATTATGATCAAGTGTAGTAGTAGATGGTCATCAGTGGATTTCA
TACAAGAGTTATTCGGTATTCGTCGTATATTGAAAT

PRETTY of: /biotmp/msa255059.2{*} February 11, 2003 08:41 ..

Table with 5 columns: sequence identifier, position 1, position 50, position 51, position 100. Rows list various msa255059.2 sequences and their consensus at specific positions.

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_090}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_A909}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_CJB110}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_H36B}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
msa255059.2{91_JM9130013}	ATATAAATTT	GGTTTAGCAT	CAGTAATTTT	AGGGTCATTC	ATAATGGTCA
Consensus	*****	*****	*****	*****	*****
	101				150
msa255059.2{91_M732}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_M781}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_COH1}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_18RS21}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_2603}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_1169NT}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_090}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_A909}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_CJB110}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_H36B}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
msa255059.2{91_JM9130013}	CAAGTCCTGT	TTTTGCGGAT	CAAACCTACAT	CGGTTCAAGT	TAATAATCAG
Consensus	*****	*****	*****	*****	*****
	151				200
msa255059.2{91_M732}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_M781}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_COH1}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_18RS21}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_2603}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_1169NT}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_090}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_A909}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_CJB110}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_H36B}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
msa255059.2{91_JM9130013}	ACAGGCCACTA	GTGTGGATGc	TAATAATTCT	TCCAATGAGA	CAAGTGCCTC
Consensus	*****	*****	*****	*****	*****
	201				250
msa255059.2{91_M732}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_M781}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_COH1}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_18RS21}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_2603}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_1169NT}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_090}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_A909}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_CJB110}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_H36B}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
msa255059.2{91_JM9130013}	AAGTGTGATT	ACTTCCAATA	ATGATAGTGT	TCAAGCGTCT	GATAAAGTTG
Consensus	*****	*****	*****	*****	*****
	251				300
msa255059.2{91_M732}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_M781}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_COH1}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_18RS21}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_2603}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_1169NT}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_090}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_A909}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_CJB110}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_H36B}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
msa255059.2{91_JM9130013}	TAAATAGTCA	AAATACGGCA	ACAAAGGACA	TTACTACTCC	TTTAGTAGAG
Consensus	*****	*****	*****	*****	*****
	301				350
msa255059.2{91_M732}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_M781}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_COH1}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_18RS21}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_2603}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_1169NT}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_090}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_A909}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_CJB110}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_H36B}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
msa255059.2{91_JM9130013}	ACAAAGCCAA	TGGTGGAAAA	AACATTACCT	GAACAAGGGA	ATTATGTTTA
Consensus	*****	*****	*****	*****	*****
	351				400
msa255059.2{91_M732}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_M781}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_COH1}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_18RS21}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_2603}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_1169NT}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_090}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_A909}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_CJB110}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_H36B}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
msa255059.2{91_JM9130013}	TAGCAAAGAA	ACCGAGGTGA	AAAATACACC	TTCAAATCA	GCCCCAGTAG
Consensus	*****	*****	*****	*****	*****
	401				450
msa255059.2{91_M732}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_M781}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_COH1}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_18RS21}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_2603}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_1169NT}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_090}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_A909}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_CJB110}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_H36B}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
msa255059.2{91_JM9130013}	CTTTCTATGC	AAAGAAAGGT	GATAAAGTTT	TCTATGACCA	AGTATTTAAT
Consensus	*****	*****	*****	*****	*****
	451				500
msa255059.2{91_M732}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_M781}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_COH1}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_18RS21}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_2603}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_1169NT}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTgGTG	GCGTACGTCG
msa255059.2{91_090}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_A909}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_CJB110}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_H36B}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
msa255059.2{91_JM9130013}	AAAGATAATG	TgAAATGGAT	TTCATATAAG	TCTTTTtGTG	GCGTACGTCG
Consensus	*****	*..*****	*****	*****-***	*****
	501				550
msa255059.2{91_M732}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_M781}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_COH1}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_18RS21}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_2603}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_1169NT}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_090}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_A909}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_CJB110}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_H36B}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
msa255059.2{91_JM9130013}	ATACGCAGCT	ATTGAGTCAC	TAGATCCATC	AGGAGGTTC	GAGACTAAAG
Consensus	*****	*****	*****	*****	*****
	551				600
msa255059.2{91_M732}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_M781}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_COH1}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_18RS21}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_2603}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_1169NT}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_090}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_A909}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_CJB110}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_H36B}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
msa255059.2{91_JM9130013}	CACCTACTCC	TGTAACAAAT	TCAGGAAGCA	ATAATCAAGA	GAAAATAGCA
Consensus	*****	*****	*****	*****	*****
	601				650
msa255059.2{91_M732}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_M781}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_COH1}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_18RS21}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_2603}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_1169NT}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_090}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_A909}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_CJB110}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_H36B}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
msa255059.2{91_JM9130013}	ACGCAAGGAA	ATTATACATT	TTACATATAA	GTAGAAGTAA	AAAATGAAGC
Consensus	*****	*****	*****	*****	*****
	651				700
msa255059.2{91_M732}	TAAGGTAGCG	AGTCCAACTC	AATTTACATT	GGCAAAGGA	GACAGAATTT
msa255059.2{91_M781}	TAAGGTAGCG	AGTCCAACTC	AATTTACATT	GGCAAAGGA	GACAGAATTT
msa255059.2{91_COH1}	TAAGGTAGCG	AGTCCAACTC	AATTTACATT	GGCAAAGGA	GACAGAATTT
msa255059.2{91_18RS21}	TAAGGTAGCG	AGTCCAACTC	AATTTACATT	GGCAAAGGA	GACAGAATTT

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_2603}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_1169NT}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_090}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_A909}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_CJB110}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_H36B}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
msa255059.2{91_JM9130013}	TAAGGTAGCG	AGTCCAAC TC	AATTTACATT	GGACAAAGGA	GACAGAATTT
Consensus	*****	*****	*****	*****	*****
701					
msa255059.2{91_M732}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_M781}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_COH1}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_18RS21}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_2603}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_1169NT}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_090}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_A909}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_CJB110}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_H36B}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
msa255059.2{91_JM9130013}	TTTACGACCA	AATACTAACT	ATTGAAGGAA	ATCAGTGGTT	ATCTTATAAA
Consensus	*****	*****	*****	*****	*****
751					
msa255059.2{91_M732}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_M781}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_COH1}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_18RS21}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_2603}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_1169NT}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_090}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_A909}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_CJB110}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_H36B}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
msa255059.2{91_JM9130013}	TCATTCAATG	GTGTTCTGTCG	TTTTGTTTTG	CTAGGTAAAG	CATCTTCAGT
Consensus	*****	*****	*****	*****	*****
801					
msa255059.2{91_M732}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_M781}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_COH1}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_18RS21}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_2603}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_1169NT}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_090}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_A909}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_CJB110}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_H36B}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
msa255059.2{91_JM9130013}	AGAAAAA ACT	GAAGATAAAG	AAAAAGTGTC	TCCTCAACCA	CAAGCCC GTA
Consensus	*****	*****	*****	*****	*****
851					
msa255059.2{91_M732}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_M781}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_COH1}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_18RS21}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_2603}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_1169NT}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_090}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_A909}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_CJB110}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_H36B}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
msa255059.2{91_JM9130013}	TTACTAAAAC	TGGTAGACTG	ACTATTTCcTA	ACGAAACAAC	TACAGGTTTT
Consensus	*****	*****	*****	*****	*****
901					
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
Consensus	*****	*****	*****	*****	*****
950					
msa255059.2{91_M732}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_M781}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_COH1}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_18RS21}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_2603}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_1169NT}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_090}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_A909}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_CJB110}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_H36B}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
msa255059.2{91_JM9130013}	GATATTTTAA	TTACGAATAT	TAAAGATGAT	AACGGTATCG	CTGCTGTTAA
Consensus	*****	*****	*****	*****	*****
951					
msa255059.2{91_M732}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_M781}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_COH1}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_18RS21}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_2603}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_1169NT}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_090}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_A909}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_CJB110}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_H36B}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
msa255059.2{91_JM9130013}	GGTACCGGTT	TGGACTGAAC	AAGGAGGGCA	AGATGATATT	AAATGGTATA
Consensus	*****	*****	*****	*****	*****
1001					
msa255059.2{91_M732}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_M781}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_COH1}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_18RS21}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_2603}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_1169NT}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_090}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_A909}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_CJB110}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_H36B}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
msa255059.2{91_JM9130013}	CAGCTGTAAC	TACTGGGGAT	GGCAACTACA	AAGTAGCTGT	ATCATTGCT
Consensus	*****	*****	*****	*****	*****
1051					
msa255059.2{91_M732}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_M781}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_COH1}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_18RS21}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_2603}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_1169NT}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_090}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_A909}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_CJB110}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_H36B}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
msa255059.2{91_JM9130013}	GACCATAAGA	ATGAGAAGGG	TCFTTATAAT	ATTCATTTAT	ACTACCAAGA
Consensus	*****	*****	*****	*****	*****
1101					
msa255059.2{91_M732}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_M781}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_COH1}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_18RS21}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_2603}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_1169NT}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_090}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_A909}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_CJB110}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_H36B}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
msa255059.2{91_JM9130013}	AGCTAGTGGG	ACACTTGTAG	GTGTAACAGG	AACTAAAGTG	ACAGTAGCTG
Consensus	*****	*****	*****	*****	*****
1151					
msa255059.2{91_M732}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_M781}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_COH1}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_18RS21}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_2603}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_1169NT}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_090}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_A909}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_CJB110}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_H36B}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
msa255059.2{91_JM9130013}	GAACTAATTC	TTCTCAAGAA	CCTATTGAAA	ATGGTTTAgC	AAAGACTGGT
Consensus	*****	*****	*****	*****	*****
1201					
msa255059.2{91_M732}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_M781}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_COH1}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_18RS21}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_2603}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_1169NT}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_090}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_A909}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_CJB110}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_H36B}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
msa255059.2{91_JM9130013}	GTTTATAATA	TTATCGGAAG	TACTGAAGTA	AAAAATGAAG	CTAAAATATC
Consensus	*****	*****	*****	*****	*****
1251					
msa255059.2{91_M732}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_M781}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_COH1}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_18RS21}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_2603}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_1169NT}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_090}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_A909}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_CJB110}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_H36B}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
msa255059.2{91_JM9130013}	AAGTCAGACC	CAATTTACTT	TAGAAAAAGG	TGACAAAATA	AATTATGATC
Consensus	*****	*****	*****	*****	*****
1301					
msa255059.2{91_M732}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_M781}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_COH1}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_18RS21}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_2603}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_1169NT}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_A909}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_CJB110}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_H36B}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
msa255059.2{91_JM9130013}	AAGTATTGAC	AGCAGATGGT	TACCAGTGGA	TTTCTTACAA	ATCTTATAGT
Consensus	*****	*****	*****	*****	*****
1351					
msa255059.2{91_M732}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_M781}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_COH1}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_18RS21}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_2603}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_1169NT}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_090}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_A909}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_CJB110}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_H36B}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
msa255059.2{91_JM9130013}	GGTGTTCGTC	GCTATATTC	TGTGAAAAAG	CTAACTACAA	GTAGTGA AAA
Consensus	*****	*****	*****	*****	*****
1401					
msa255059.2{91_M732}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_M781}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_COH1}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_18RS21}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_2603}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_1169NT}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_090}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_A909}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_CJB110}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_H36B}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
msa255059.2{91_JM9130013}	AGCGAAAGAT	GAGGCGACTA	AACCGACTAG	TTATCCCAAC	TTACCTAAAA
Consensus	*****	*****	*****	*****	*****
1451					
msa255059.2{91_M732}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_M781}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_COH1}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_18RS21}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_2603}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_1169NT}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_090}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_A909}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_CJB110}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_H36B}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
msa255059.2{91_JM9130013}	CAGGTACCTA	TACATTTACT	AAAACCTGTAG	ATGTGAAaAG	TCAACCTAAA
Consensus	*****	*****	*****	*****	*****
1501					
msa255059.2{91_M732}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_M781}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_COH1}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_18RS21}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_2603}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_1169NT}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_090}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_A909}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_CJB110}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_H36B}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
msa255059.2{91_JM9130013}	GTATCAAGTC	CAGTGGAAIT	TAATTTTCAA	AAGGGTGAAA	AAATACAITA
Consensus	*****	*****	*****	*****	*****
1551					
msa255059.2{91_M732}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
1600					

Table 89: Comparative Sequences relating to SAG1350

msa255059.2{91_M781}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_COH1}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_18RS21}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_2603}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_1169NT}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_090}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_A909}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_CJB110}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_H36B}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
msa255059.2{91_JM9130013}	TGATCAAGTG	TTAGTAGTAG	ATGGTCATCA	GTGGATTCA	TACAAGAGTT
Consensus	*****	*****	*****	*****	*****

msa255059.2{91_M732}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT	1601	1629
msa255059.2{91_M781}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_COH1}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_18RS21}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_2603}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_1169NT}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_090}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_A909}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_CJB110}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_H36B}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
msa255059.2{91_JM9130013}	ATTCCGGTAT	TCGTCGCTAT	ATTGAAATT		
Consensus	*****	*****	*****		

SEQ ID NO. 8912

STRAIN 2603 frame: 1

MKKGQVNDTKQSYSLRKYKFLGLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSSNETSASSVITSNNDVSVQASDKVVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKETEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFVCGVRRYAAIESLDPGGSEETKAPTPVINSNGSNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLTKGDRIFDYDQILTIIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPOQARITKTGRLTISNETTTGFDILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNVYKVAVSFADHKNEKGLYNIHLYYQEAAGTLLVGVTTGKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNLPKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYIEI

SEQ ID NO. 8913

STRAIN 090 frame: 1

KKGQVNDTKQSYSLRKYKFLGLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSSNETSASSVITSNNDVSVQASDKVVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKETEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFVCGVRRYAAIESLDPGGSEETKAPTPVINSNGSNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLTKGDRIFDYDQILTIIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPOQARITKTGRLTISNETTTGFDILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNVYKVAVSFADHKNEKGLYNIHLYYQEAAGTLLVGVTTGKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNLPKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYIEI

SEQ ID NO. 8914

STRAIN A909 frame: 1

KKGQVNDTKQSYSLRKYKFLGLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSSNETSASSVITSNNDVSVQASDKVVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKETEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFVCGVRRYAAIESLDPGGSEETKAPTPVINSNGSNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLTKGDRIFDYDQILTIIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPOQARITKTGRLTISNETTTGFDILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNVYKVAVSFADHKNEKGLYNIHLYYQEAAGTLLVGVTTGKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNLPKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYIEI

SEQ ID NO. 8915

STRAIN H36B frame: 1

KKGQVNDTKQSYSLRKYKFLGLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSSNETSASSVITSNNDVSVQASDKVVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKETEVKNTPSKSAPVAFYAKKGDVVFYDQVFNKDNVQWISYKSFVCGVRRYAAIESLDPGGSEETKAPTPVINSNGSNQEKIATQGNVTFSHKVEVKNEAKVASPTQFTLTKGDRIFDYDQILTIIEGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPOQARITKTGRLTISNETTTGFDILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTTGDNVYKVAVSFADHKNEKGLYNIHLYYQEAAGTLLVGVTTGKVTVAGTNSSQEPIENGLAKTGVYNIIGSTEVEKNEAKISSQTQFTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNLPKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHVDQVLVVDGHWISYKSYSGIRRYIEI

SEQ ID NO. 8916

STRAIN 18RS21 frame: 1

KKGQVNDTKQSYSLRKYKFLGLASVILGSFIMVTSPPVFADQTTTSVQVNNQGTGSVDANNSSNETSASSVITSNNDVSVQASDKVVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYYSKET

Table 89: Comparative Sequences relating to SAG1350

EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSE
TKAPTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVGTGKVTVAGTNSSQEPIENGLAKTGVYNI IGSTEVKNEAKI SSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8917

STRAIN M732 frame: 1

QVNDTKQSYSLRKYKFLASVILGSFIMVTSVPVFADQTTSVQVNNQTGTSVDANSSNET
SASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETEVEK
NTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSETKA
PTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI EGN
QWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD ILI
TNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNIHLY
YQEASGTLVGVGTGKVTVAGTNSSQEPIENGLPKTGVYNI IGSTEVKNEAKI SSQTQFTL
EKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNLPKT
GTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYIEI

SEQ ID NO. 8918

STRAIN COH1 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSVPVFADQTTSVQVNNQTGTSVDANSS
NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETE
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSE
TKAPTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVGTGKVTVAGTNSSQEPIENGLPKTGVYNI IGSTEVKNEAKI SSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8919

STRAIN M781 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSVPVFADQTTSVQVNNQTGTSVDANSS
NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETE
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSE
TKAPTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVGTGKVTVAGTNSSQEPIENGLPKTGVYNI IGSTEVKNEAKI SSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8920

STRAIN CJB110 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSVPVFADQTTSVQVNNQTGTSVDANSS
NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETE
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSE
TKAPTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVGTGKVTVAGTNSSQEPIENGLAKTGVYNI IGSTEVKNEAKI SSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8921

STRAIN 1169NT frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSVPVFADQTTSVQVNNQTGTSVDANSS
NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETE
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSE
TKAPTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVGTGKVTVAGTNSSQEPIENGLAKTGVYNI IGSTEVKNEAKI SSQTQ
FTLEKGDKINVDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDVKSQPKVSSPVEFNFQKGEKIHYDQVLVVDGHQWISYKSYSGIRRYI
EI

SEQ ID NO. 8922

STRAIN JM9130013 frame: 1

KKGQVNDTKQSYSLRKYKFLASVILGSFIMVTSVPVFADQTTSVQVNNQTGTSVDANSS
NETSASSVITSNNDSVQASDKVNSQNTATKDIITPLVETKPMVEKTLPEQGNVYVSKETE
EVKNTPSKSAPVAFYAKKGDKVFYDQVFNKDNVWKWISYKSFVCGVRRYAAIESLDPSSGGSE
TKAPTPTVNSGNSNNQEKIATQGNVYTFSHKVEVKNEAKVASPTQFTLDKGDRI FVDQILTI
EGNQWLSYKSFNGVRRFVLLGKASSVEKTEDKEKVSPPQARITKTGRLTISNETTTGFD
ILITNIKDDNGIAAVKVPVWTEQGGQDDIKWYTAVTGDDGNYKVAVSFADHKNEKGLYNI
HLYYQEASGTLVGVGTGKVTVAGTNSSQEPIENGLAKTGVYNI IGSTEVKNEAKI SSQTQ

Table 89: Comparative Sequences relating to SAG1350

FTLEKGDKINYDQVLTADGYQWISYKSYSGVRRYIPVKKLTTSSEKAKDEATKPTSYPNL
PKTGTYYTFTKTVDKVKSQPKVSSPFVEFNFQKGEKIHVDQVLVVDGHQWISYKSYSGIRRYI
EI

PRETTY of: /biotmp/msa255178.2(*) February 11, 2003 08:51 ..

Table with 5 columns: Accession, Position 1, Position 50, Position 100, Position 150. Rows include msa255178.2{91_090} through msa255178.2{91_1169NT} and a Consensus row.

Table with 5 columns: Accession, Position 51, Position 100, Position 150, Position 200. Rows include msa255178.2{91_090} through msa255178.2{91_1169NT} and a Consensus row.

Table with 5 columns: Accession, Position 101, Position 150, Position 200, Position 250. Rows include msa255178.2{91_090} through msa255178.2{91_1169NT} and a Consensus row.

Table with 5 columns: Accession, Position 151, Position 200, Position 250, Position 300. Rows include msa255178.2{91_090} through msa255178.2{91_1169NT} and a Consensus row.

Table with 5 columns: Accession, Position 201, Position 250, Position 300, Position 350. Rows include msa255178.2{91_090} through msa255178.2{91_1169NT} and a Consensus row.

Table with 5 columns: Accession, Position 251, Position 300, Position 350, Position 400. Rows include msa255178.2{91_090} through msa255178.2{91_1169NT} and a Consensus row.

Table 89: Comparative Sequences relating to SAG1350

msa255178.2{91_H36B}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSFPQ	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_JM9130013}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSFPQ	QARITKTGRL	TIyNETTTGF
msa255178.2{91_COH1}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSFPQ	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_M781}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSFPQ	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_M732}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSFPQ	QARITKTGRL	TI\$NETTTGF
msa255178.2{91_1169NT}	SFNGVRRFVL	LGKASSVEKT	EDKEKVSFPQ	QARITKTGRL	TI\$NETTTGF
Consensus	*****	*****	*****	*****	*_*-*****
301					
msa255178.2{91_090}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_18RS21}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_2603}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_A909}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_CJB110}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_H36B}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_JM9130013}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_COH1}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_M781}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_M732}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
msa255178.2{91_1169NT}	DILITNIKDD	NGIAAVKVPV	WTEQGGQDDI	KWYTAVTTGD	GNYKVAVSFA
Consensus	*****	*****	*****	*****	*****
351					
msa255178.2{91_090}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_18RS21}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_2603}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_A909}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_CJB110}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_H36B}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_JM9130013}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_COH1}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M781}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_M732}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
msa255178.2{91_1169NT}	DHKNEKGLYN	IHLYYQEASG	TLVGVGTGTV	TVAGTNSSQE	PIENGLaKTG
Consensus	*****	*****	*****	*****	*****_***
401					
msa255178.2{91_090}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_18RS21}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_2603}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_A909}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_CJB110}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_H36B}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_JM9130013}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_COH1}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M781}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_M732}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
msa255178.2{91_1169NT}	VYNIIGSTEV	KNEAKISSQT	QFTLEKGDKI	NYDQVLTADG	YQWISYKSYS
Consensus	*****	*****	*****	*****	*****
451					
msa255178.2{91_090}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_18RS21}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_2603}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_A909}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_CJB110}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_H36B}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_JM9130013}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_COH1}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M781}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_M732}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
msa255178.2{91_1169NT}	GVERRYPVKK	LTTSSSEKAKD	EATKPTSYPN	LPKGTGYTFT	KTVDVKSQPK
Consensus	*****	*****	*****	*****	*****
501					
msa255178.2{91_090}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_18RS21}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_2603}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_A909}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_CJB110}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_H36B}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_JM9130013}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_COH1}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M781}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_M732}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
msa255178.2{91_1169NT}	VSSPVEFNQ	KGEKIHVDQV	LVVDGHWIS	YKSYSGIRRY	IEI
Consensus	*****	*****	*****	*****	***

CLAIMS:

1. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is
5 encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of both GAS and *Streptococcus pneumoniae*.
2. The immunogenic composition of claim 1, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 1.
3. An immunogenic composition comprising a combination of GBS polypeptides, said
10 combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of GAS.
4. The immunogenic composition of claim 3, wherein said GBS polypeptides are encoded by GBS polynucleotide sequences selected from GBS Subset 2.
- 15 5. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS polynucleotide sequence which is homologous to a polynucleotide sequence of *Streptococcus pneumoniae*.
6. The immunogenic composition of claim 5, wherein said GBS polypeptides are encoded
20 by GBS polynucleotide sequences selected from GBS Subset 3.
7. An immunogenic composition comprising a combination of GBS polypeptides, said combination consisting of two, three, four or five polypeptides, wherein each polypeptide is encoded by a GBS serotype polynucleotide sequence which is homologous to at least one other GBS serotype.
- 25 8. The immunogenic composition of claim 2, 4 or 6, wherein one or more of the GBS polypeptides are encoded by GBS serotype polynucleotide sequences which are homologous to at least one other GBS serotype.
9. An immunogenic composition comprising a fusion protein, wherein said fusion protein comprises a first polypeptide sequence which is encoded by a GBS serotype polynucleotide
30 which is conserved across one or more GBS serotypes.
10. A polynucleotide sequence, or a fragment comprising at least 10 contiguous polynucleotides, selected from the sequences set forth on Tables 13 – 31 and 40 – 89.
11. The polynucleotide fragment of claim 10, wherein said fragment is derived from a GBS serotype polynucleotide sequence and is homologous to at least one additional GBS serotype
35 polynucleotide sequence.

Figure 1

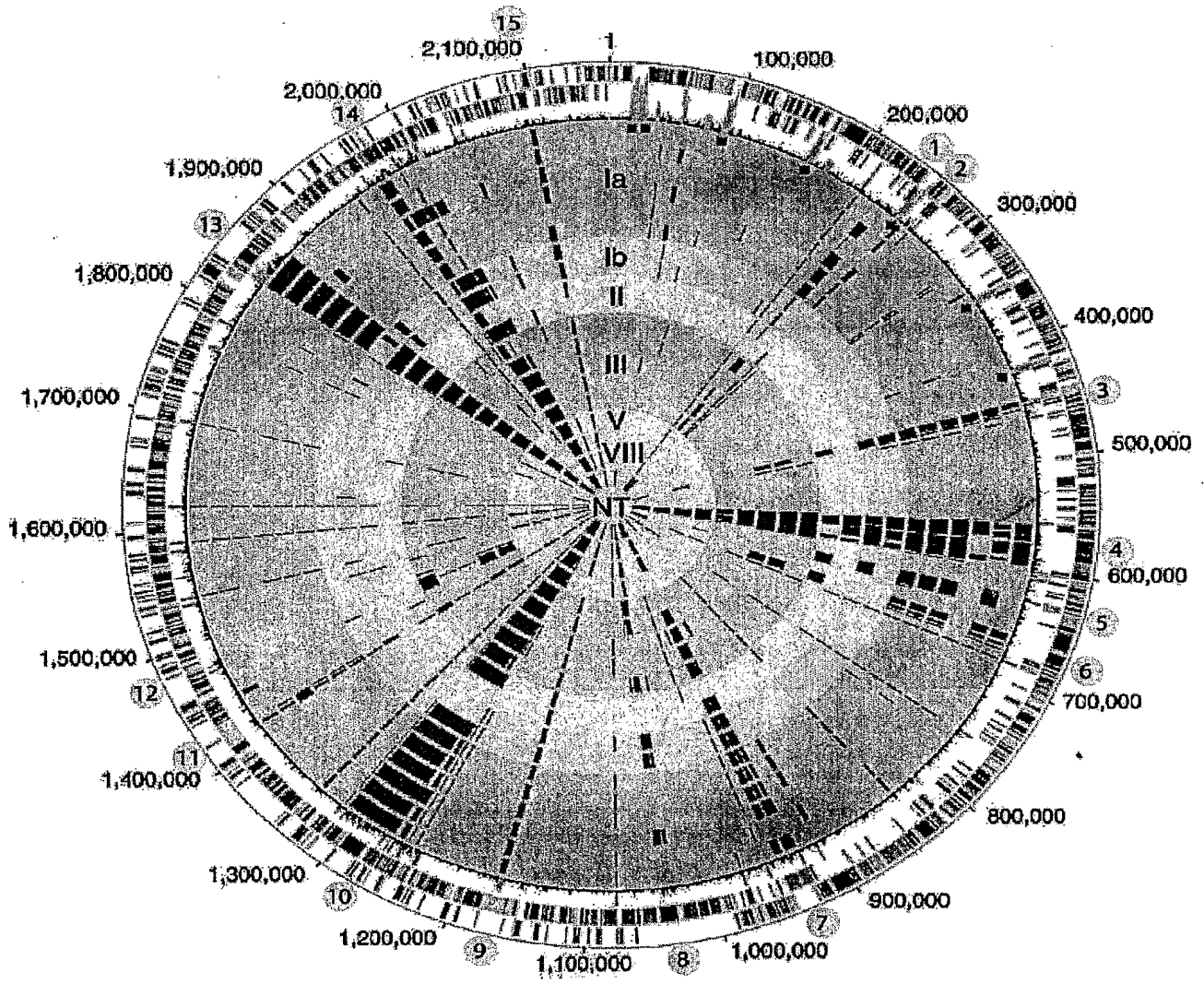


Figure 2

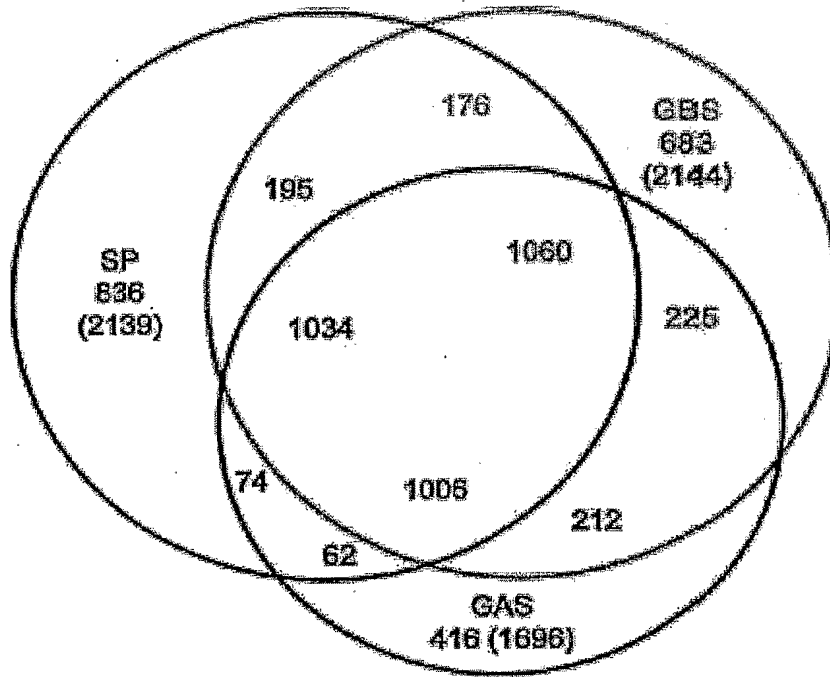
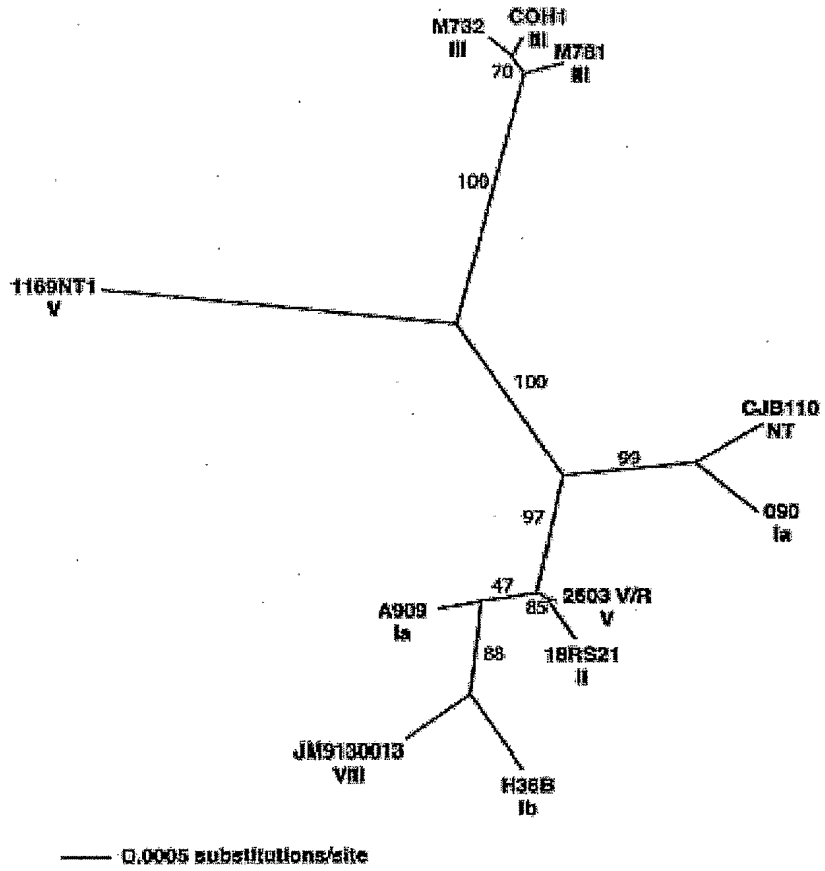


Figure 3





Strains:
Serotype:

V 2603 V/R
III NT81
III NT32
III C91
Ia A909
Ib (S7)757b
Ia 515
Ia DKL
Ia D88
Ia DAVIS
II DZ1
III C910
III D136C
III C911
Ia 090
VIII S20014
VIII 389130013
V C911
Ib R568
II 18821



Cluster 1: 6 ORFs
Cluster 2: 7 ORFs
Cluster 3: 15 ORFs
Cluster 4: 7 ORFs
1698 ORFs shared by all strains
Cluster 5: 11 ORFs
Cluster 6: 5 ORFs
Cluster 7: 6 ORFs
Cluster 8: 6 ORFs
Cluster 9: 17 ORFs
Cluster 10: 18 ORFs
Cluster 11: 92 ORFs unique to strain 2603 V/R
Cluster 12: 5 ORFs
Cluster 13: 14 ORFs
Cluster 14: 15 ORFs
Cluster 15: 31 ORFs
Cluster 16: 45 ORFs

FIGURE 5